

OM protein - protein search, using sw model

Run on: February 4, 2006, 03:43:49 ; Search time 8.44444 Seconds
 16.652 Million cell updates/sec

Title: US-10-790-768A-1

Perfect score: 58

Sequence: 1 RKLMLKSTRQR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqB, 11718660 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA New:*

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2: /cgn2_6/pctodata/2/pubpaa/us06_NEW_PUB_pep:*

3: /cgn2_6/pctodata/2/pubpaa/us07_NEW_PUB_pep:*

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8: /cgn2_6/pctodata/2/pubpaa/us60_NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	37	63.8	54	7 US-11-150-054A-13
2	37	63.8	54	7 US-11-150-054A-21
3	37	63.8	54	7 US-11-150-054A-26
4	34	58.6	327	7 US-11-165-211-52
5	34	58.6	327	7 US-11-165-226-62
6	32	55.2	211	7 US-11-214-199-60
7	32	55.2	212	7 US-11-214-199-4
8	32	55.2	212	7 US-11-214-199-12
9	32	55.2	411	7 US-11-092-168-8
10	32	55.2	672	6 US-10-689-742-70
11	31	53.4	27	7 US-11-078-469-32
12	31	53.4	28	7 US-11-078-469-33
13	31	53.4	30	7 US-11-078-469-24
14	31	53.4	30	7 US-11-078-469-62
15	31	53.4	119	7 US-11-120-308-146
16	31	53.4	183	6 US-10-467-657-44
17	31	53.4	183	6 US-10-467-657-8498
18	31	53.4	277	7 US-11-120-308-150
19	31	53.4	280	6 US-10-821-234-1300
20	31	53.4	388	7 US-11-082-389-220
21	31	53.4	407	7 US-11-051-267-25
22	31	53.4	566	7 US-11-033-039-1244
23	31	53.4	580	7 US-11-054-281-95
24	31	53.4	1029	6 US-10-821-234-908
25	30	51.7	7 US-11-016-542-12	

ALIGNMENTS

SEQ ID	NO.	TYPE: PT	LENGTH: 54	SEQUENCE
1	US-11-150-054A-13	OTHER INFORMATION: synthetic peptide	54	RKLMLKSTRQR
2	US-11-150-054A-21	FEATURE: OTHER INFORMATION: artificial sequence	54	RKLMLKSTRQR
3	US-11-150-054A-26	ORGANISM: Wilkinson, Jack Q.	54	RKLMLKSTRQR
4	US-11-165-211-52	GENERAL INFORMATION:	54	RKLMLKSTRQR
5	US-11-165-226-62	APPLICANT: Wilkinson, Jack Q.	54	RKLMLKSTRQR
6	US-11-214-199-60	TITLE OF INVENTION: Plasmid Transit Peptides	54	RKLMLKSTRQR
7	US-11-214-199-4	FILE REFERENCE: 219-428US1	54	RKLMLKSTRQR
8	US-11-214-199-12	CURRENT APPLICATION NUMBER: US/11/150,054A	54	RKLMLKSTRQR
9	US-11-092-168-8	PRIOR APPLICATION NUMBER: 60/578,535	54	RKLMLKSTRQR
10	US-10-689-742-70	PRIOR FILING DATE: 2004-06-09	54	RKLMLKSTRQR
11	US-11-078-469-32	NUMBER OF SEQ ID NOS: 57	54	RKLMLKSTRQR
12	US-11-078-469-33	SOFTWARE: PatentIn version 3.3	54	RKLMLKSTRQR
13	US-11-078-469-24	SEQ ID NO: 13	54	RKLMLKSTRQR
14	US-11-078-469-62	LENGTH: 54	54	RKLMLKSTRQR
15	US-11-120-308-146	TYPE: PT	54	RKLMLKSTRQR
16	US-10-467-657-44	ORGANISM: Wilkinson, Jack Q.	54	RKLMLKSTRQR
17	US-10-467-657-8498	GENERAL INFORMATION:	54	RKLMLKSTRQR
18	US-11-120-308-150	APPLICANT: Wilkinson, Jack Q.	54	RKLMLKSTRQR
19	US-10-821-234-1300	TITLE OF INVENTION: Plasmid Transit Peptides	54	RKLMLKSTRQR
20	US-11-082-389-220	FILE REFERENCE: 219-428US1	54	RKLMLKSTRQR
21	US-11-051-267-25	CURRENT APPLICATION NUMBER: US/11/150,054A	54	RKLMLKSTRQR
22	US-11-033-039-1244	PRIOR APPLICATION NUMBER: 60/578,535	54	RKLMLKSTRQR
23	US-11-054-281-95	PRIOR FILING DATE: 2004-06-09	54	RKLMLKSTRQR
24	US-10-821-234-908	NUMBER OF SEQ ID NOS: 57	54	RKLMLKSTRQR
25	US-11-016-542-12	SOFTWARE: PatentIn version 3.3	54	RKLMLKSTRQR

SEQ ID NO: 21

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; LENGTH: 54
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE: OTHER INFORMATION: synthetic peptide
US-11-150-054A-21
Query Match 63.8%; Score 37; DB 7; Length 54;
Best Local Similarity 58.3%; Pred. No. 1;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRQR 12
Db 34 RRFNRNTRQR 45
RESULT 3
US-11-150-054A-26
Sequence 26, Application US/11150054A
Publication No. US20050278801A1
; GENERAL INFORMATION:
; APPLICANT: KOMA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
; FILE REFERENCE: 4033-13
; CURRENT APPLICATION NUMBER: US/11-165, 226
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JPP004-189007
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 62
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-226-62
Query Match 58.6%; Score 34; DB 7; Length 327;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 KSTRQR 11
Db 124 KSTRQR 130
RESULT 4
US-11-150-054A-26
US-11-150-054A-26
; LENGTH: 54
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE: OTHER INFORMATION: synthetic peptide
US-11-150-054A-26
Query Match 63.8%; Score 37; DB 7; Length 54;
Best Local Similarity 58.3%; Pred. No. 1;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRQR 12
Db 34 RRFNRNTRQR 45
RESULT 5
US-11-165-226-62
Sequence 62, Application US/11165226
Publication No. US2005028762A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
; FILE REFERENCE: 4033-13
; CURRENT APPLICATION NUMBER: US/11-165, 226
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JPP004-189007
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 62
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-226-62
Query Match 58.6%; Score 34; DB 7; Length 327;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 KSTRQR 11
Db 124 KSTRQR 130
RESULT 6
US-11-214-199-10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human
; FEATURE: OTHER INFORMATION: synthetic peptide
US-11-214-199-10
Query Match 55.2%; Score 22; DB 7; length 211;
Best Local Similarity 58.3%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRQR 12
Db 159 RRMIGAPLRR 170

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RESULT 7
US-11-214-199-4
Sequence 4, Application US/11214199
Publication No. US2006003377A1
GENERAL INFORMATION:
APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, Warren S
APPLICANT: VINEY, Elizabeth M
APPLICANT: WILSON, Tracey A
APPLICANT: RICHARDSON, Rachael T
APPLICANT: STARR, Robyn
APPLICANT: NICHOLSON, Sandra E
APPLICANT: METCALF, Donald
APPLICANT: NICOLA, Nicos A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS
FILE REFERENCE: 10972A
CURRENT APPLICATION NUMBER: US/11/214,199
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/302,769
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: Mouse
US-11-214-199-4

RESULT 8
Sequence 12, Application US/11214199
Publication No. US2006003377A1
GENERAL INFORMATION:
APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, Warren S
APPLICANT: VINEY, Elizabeth M
APPLICANT: WILSON, Tracey A
APPLICANT: RICHARDSON, Rachael T
APPLICANT: STARR, Robyn
APPLICANT: NICHOLSON, Sandra E
APPLICANT: METCALF, Donald
APPLICANT: NICOLA, Nicos A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS
TITLE OF INVENTION: BOX
FILE REFERENCE: 10972A
CURRENT APPLICATION NUMBER: US/11/214,199
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/302,769
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 212
TYPE: PRT
ORGANISM: Rat
US-11-214-199-12

Query Match 55.2%; Score 32; DB 7; Length 212;
Best Local Similarity 58.3%; Pred. No. 35; Mismatches 2; Indels 0; Gaps 0;
Matches 7;

Qy 1 RKMJKSTRRRR 12
Db 160 RRMIGAPLRGR 171

RESULT 9
US-11-092-168-8
Sequence 8, Application US/11092168
Publication No. US20050277658A1
GENERAL INFORMATION:
APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Hurley, Laurence H.
APPLICANT: Manadevan, Daruka
APPLICANT: Han, Halyong
APPLICANT: Bears, David J.
APPLICANT: Vanikayalapati, Hariprasad
APPLICANT: Basiyam, Sridevi
APPLICANT: Munoz, Ruben M.
APPLICANT: Warner, Steven L.
APPLICANT: Della Croce, Kimiko
APPLICANT: Von Hoff, Daniel D.
APPLICANT: Grand, Cory L.
TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
FILE REFERENCE: 9_0214_00003CONT3
CURRENT APPLICATION NUMBER: US/11/092,168
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US 10/965,313
US 60/608,529
US 60/511,486
US 60/511,489
PRIOR FILING DATE: 2004-10-14
2004-09-09
2003-10-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-11-092-168-8

Query Match 55.2%; Score 32; DB 7; Length 411;
Best Local Similarity 87.5%; Pred. No. 72; Mismatches 1; Indels 0; Gaps 0;
Matches 7;

Qy 2 KMLKSTAR 9
Db 43 KMLKSTAR 50

RESULT 10
US-10-689-742-70
Sequence 70, Application US/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavallie, Edward R
APPLICANT: Racine, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Tracy, Maurice
APPLICANT: Spaulding, Vicki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766_000091.10
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR FILING DATE: 2000-12-21

Query Match 55.2%; Score 32; DB 7; Length 212;
Best Local Similarity 58.3%; Pred. No. 35;

NUMBER OF SEQ ID NOS: 231
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 70
 LENGTH: 672
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (107)..(107)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (111)..(111)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (117)..(118)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (645)..(645)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-10-689-742-70

Query Match 55 2%; Score 32; DB 6; Length 672;
 Best Local Similarity 50 0%; Pred. No. 1.2e+02; Mismatches 6; Conservatve 4; Indels 0; Gaps 0;
 Matches 6; Other Information: Xaa can be any naturally occurring amino acid

Qy 1 RKMILKSTRQR 12
 Db 598 RKLLEBGRRSR 609

RESULT 11
 US-11-078-469-32
 Publication No. US20050282755A1
 GENERAL INFORMATION:
 APPLICANT: HART, SCOTT A.
 APPLICANT: ZEH, KARIN
 APPLICANT: MACHEIDT, THOMAS
 APPLICANT: STOLOW, DAVID
 APPLICANT: CONGER, DEE
 TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
 LENGTH: 28
 FILE REFERENCE: ANS-2001-UT
 CURRENT APPLICATION NUMBER: US/11/078, 469
 PRIOR FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: 60/554, 526
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO: 33
 LENGTH: 28
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (1)
 OTHER INFORMATION: Ac-Thr

US-11-078-469-33
 Sequence 32, Application US/11078469
 Publication No. US20050282755A1
 CURRENT APPLICATION NUMBER: US/11/078, 469
 PRIOR FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: 60/554, 526
 PRIOR FILING DATE: 2004-10-15
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO: 32
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (1)
 OTHER INFORMATION: Ac-Thr

US-11-078-469-32

Query Match 53 4%; Score 31; DB 7; Length 28;
 Best Local Similarity 41.7%; Pred. No. 6.1%; Mismatches 5; Conservatve 4; Indels 3; Gaps 0;
 Matches 5; Other Information: Peptide moiety

Qy 1 RKMILKSTRQR 12
 Db 16 RKMRAARRRR 27

RESULT 13
 US-11-078-469-24
 Sequence 24, Application US/11078469
 Publication No. US20050282755A1
 GENERAL INFORMATION:
 APPLICANT: HART, SCOTT A.
 APPLICANT: ZEH, KARIN
 APPLICANT: MACHEIDT, THOMAS
 APPLICANT: STOLOW, DAVID
 APPLICANT: CONGER, DEE
 TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
 LENGTH: 28
 FILE REFERENCE: ANS-2001-UT
 CURRENT APPLICATION NUMBER: US/11/078, 469
 PRIOR FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: 60/554, 526
 PRIOR FILING DATE: 2004-10-15
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO: 24
 LENGTH: 30
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Qy 1 RKMILKSTRQR 12

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; OTHER INFORMATION: peptide moiety
; FEATURE: NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Ac-Thr
US-11-078-465-24

Query Match      53.4%; Score 31; DB 7; Length 30;
Best Local Similarity 41.7%; Pred. No. 6.6;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy          1 RKLKSTRQR 12
Db          16 RNFMRARRRR 27

RESULT 14
US-11-078-469-62
Sequence 62, Application US/11078469
Publication No. US20050282755A1
GENERAL INFORMATION:
APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHELEIT, THOMAS
APPLICANT: STOLOW, DAVID
APPLICANT: CONGER, DEB
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 62
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide moiety
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Ac-Thr
US-11-078-469-62

RESULT 15
US-11-120-308-146
Query Match      53.4%; Score 31; DB 7; Length 30;
Best Local Similarity 41.7%; Pred. No. 6.6;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy          1 RKLKSTRQR 12
Db          16 RNFMRARRRR 27

RESULT 15
US-11-120-308-146
Sequence 62, Application US/11120308
Publication No. US2006005277A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: cDNAs Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 146
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-120-308-146

Query Match      53.4%; Score 31; DB 7; Length 119;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy          4 LKSTRQR 12
Db          41 MKRTRDRR 49

Search completed: February 4, 2006, 03:47:58
Job time : 9.44444 secs

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OM protein - protein search, using sw model									
Run on:	February 4, 2006, 03:26:33 ; Search time 248.444 seconds								
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Perfect score:	58 1 RKMKMKTRQR 12								
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5								
Searched:	2443163 seqb, 439378781 residues								
Total number of hits satisfying chosen parameters:	2443163								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description					
1	58	100.0	12	8 ADS17617	RESULT 1 ADS17617				
2	58	100.0	15	8 ADS17632	ID	ADS17617 standard; peptide; 12 AA.			
3	58	100.0	15	8 ADS17630	XX				
4	58	100.0	15	8 ADS17618	AC	ADS17617;			
5	58	100.0	21	8 ADS17636	XX				
6	58	100.0	21	8 ADS17620	DT	02-DEC-2004 (first entry)			
7	58	100.0	21	8 ADS17635	XX				
8	58	100.0	27	8 ADS17621	XX				
9	48	82.8	19	8 ADS17634	PP	04-MAR-2004; 2004WO-US006445.			
10	48	82.8	25	8 ADS17638	PR	04-MAR-2003; 2003US-0451243P.			
11	48	82.8	25	8 ADS17637	XX	03-MAR-2004; 2004US-00790768.			
12	43	74.1	63	4 AAU50525	PA	(BIOW-) BIOMHITTAKER TECHNOLOGIES INC.			
13	43	74.1	63	6 ABM17044	PI	Karas M;			
14	43	74.1	247	7 ADT70413	XX				
15	42	72.4	33	4 AAG90210	PT	WPI: 2004-653708/63.			
16	39	67.2	33	5 ABU05628	PT	New isolated and purified polypeptide with a protein transduction domain, useful for delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell.			
17	39	67.2	33	5 ABU05754	PT				
18	39	67.2	84	4 AAU53875	XX				
19	39	67.2	84	6 ABM0394	PS	Claim 1; SEQ ID NO 1; 60pp; English.			
20	39	67.2	93	4 AAU63362	CC	The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PBD-cargo moiety complexes that can reversibly immortalise			
21	39	67.2	93	4 AAU67333	CC	cells and increase cell viability in culture. The present sequence is a reverse isomer of ADS17641, a previously identified internalising peptide.			
22	39	67.2	93	6 ABM03852	CC				
23	39	67.2	93	6 ABM59881	CC				
24	39	67.2	131	3 AAG04024	SQ	Sequence 12 AA;			

Query Match 100.0%; Score 58; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0063; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLMLKSTRQR 12
 1 RKLMLKSTRQR 12

Db 4 RKLMLKSTRQR 15

RESULT 2
 ID ADS17632
 ID ADS17632 standard; peptide; 15 AA.
 XX
 AC ADS17632;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Amino acid sequence of a PTD designated Biotin-Lys-Ingres.
 XX protein transduction domain; PTD; PTD-cargo moiety complex;
 KW cell immortalisation; cell viability; internalising peptide;
 KW cell transport.

XX
 OS Synthetic.

XX
 FH Key
 FT Modified-site 1
 FT /note= "biotin attached"
 XX
 PN WO2004078933-A2.
 XX
 PD 16-SEP-2004.
 XX
 PR 04-MAR-2004; 2004WO-US006445.
 XX
 PR 04-MAR-2003; 2003US-0451243P.
 XX
 PR 03-MAR-2004; 2004US-00790768.

(BIOW-) BIOWHITTAKER TECHNOLOGIES INC.
 PT Karas M;
 XX
 DR WPI; 2004-653708/63.
 XX
 PT New isolated and purified polypeptide with a protein transduction domain,
 PT useful for delivering small molecules, proteins and nucleic acids to an
 PT intracellular compartment of a cell.

XX
 PS Example 4; SEQ ID NO 14; 60PP; English.

XX
 CC The specification describes peptides which function as a protein
 CC transduction domain (PTD), and are capable of delivering small molecules,
 CC proteins, and nucleic acids to an intracellular compartment of a cell. An
 CC amino terminal lysine linker improves the efficiency of the PTD. The PTD
 CC can be used in PTD-cargo moiety complexes that can reversibly immortalise
 CC cells and increase cell viability in culture. The present Sequence
 CC represents PTD peptide used in an experiment to determine the
 CC transduction efficiency of inverted isomers of PTDs.

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 58; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0078; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLMLKSTRQR 12
 1 RKLMLKSTRQR 12

Db 4 RKLMLKSTRQR 15

RESULT 4
 ID ADS17618
 ID ADS17618 standard; peptide; 15 AA.
 XX
 AC ADS17618;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Amino acid sequence of protein transduction domain (PTD) peptide #2.
 XX protein transduction domain; PTD; PTD-cargo moiety complex;
 KW cell immortalisation; cell viability; internalising peptide;
 KW cell transport.

XX
 RESULT 3
 ADS17630

OS Synthetic.
 XX
 PN WO2004078933-A2.
 XX
 PD 16-SEP-2004.
 XX
 PR 04-MAR-2004; 2004WO-US006445.
 XX
 PR 03-MAR-2003; 2003US-0451243P.
 XX
 PR 03-MAR-2004; 2004US-00790768.
 XX
 PA (BIOW-) BIOWHITTAKER TECHNOLOGIES INC.
 XX
 PT useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
 XX
 PR Example 10; SEQ ID NO 20; 60pp; English.
 XX
 CC The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS1634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.
 CC
 CC transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker.
 XX
 Sequence 15 AA;
 Query Match 100.0%; Score 58; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0078; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Oy 1 RKLMLKSTRQR 12
 DB 4 RKLMLKSTRQR 15
 RESULT 5
 ADS17636
 ID ADS17636 Standard; peptide; 21 AA.
 XX
 AC ADS17636;
 XX
 DT 02-DEC-2004 (first entry)
 DB Amino acid sequence of a PTD designated peptide 15.
 XX
 KW protein transduction domain; PTD; PTD-cargo moiety complex; KW cell immortalisation; cell viability; internalising peptide; KW cell transport.
 XX
 OS Synthetic.
 XX
 PN WO2004078933-A2.
 XX
 PD 16-SEP-2004.
 XX
 PR 04-MAR-2004; 2004WO-US006445.
 XX
 PR 03-MAR-2003; 2003US-0451243P.
 XX
 PR 03-MAR-2004; 2004US-00790768.
 XX
 PA (BIOW-) BIOWHITTAKER TECHNOLOGIES INC.
 XX
 PT Karas M.;
 XX
 PR Karas M.;
 XX
 WPI; 2004-653708/63.
 XX
 PT New isolated and purified polypeptide with a protein transduction domain, PT useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
 XX
 PR Example 10; SEQ ID NO 20; 60pp; English.
 XX
 CC The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise

CC	cells and increase cell viability in culture. The present PTD has a lysine linker and a nuclear localisation signal.
CC	
XX	
SQ	Sequence 21 AA;
	Query Match 100.0%; Score 58; DB 8; Length 21;
	Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RKLMLKSTRRQR 12
Db	4 RKLMLKSTRRQR 15
	RESULT 7
ID	ADS17635
ID	ADS17635 standard; peptide; 21 AA.
XX	
AC	ADS17635;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Amino acid sequence of a PTD designated peptide 14.
XX	
KW	protein transduction domain; PTD; PTD-cargo moiety complex;
KW	cell immortalisation; cell viability; internalising peptide;
KW	cell transport.
XX	
OS	Synthetic.
XX	
FH	Location/Qualifiers
FT	Modified-site 1 /note= "biotin attached"
XX	
PN	WO2004078933-A2.
PD	16-SEP-2004.
XX	
PP	04-MAR-2004; 2004WO-US006445.
XX	
PR	04-MAR-2003; 2003US-0451243P.
PR	03-MAR-2004; 2004US-00790768.
XX	
PA	(BIOW-) BIOWHITTAKER TECHNOLOGIES INC.
PA	
PA	Karas M;
XX	
DR	WPI; 2004-653708/63.
XX	
PT	New isolated and purified polypeptide with a protein transduction domain, PT useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
XX	
PS	Disclosure; SEQ ID NO 5; 60pp; English.
XX	
CC	The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal Lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker and 2 nuclear localisation signals.
CC	
XX	
DR	Sequence 27 AA;
XX	
PT	Query Match 100.0%; Score 58; DB 8; Length 27;
PT	Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
XX	
PS	Example 10; SEQ ID NO 19; 60pp; English.
XX	
CC	The specification describes Peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal Lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.
CC	
XX	
SQ	Sequence 21 AA;
	Query Match 100.0%; Score 58; DB 8; Length 21;
	Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RKLMLKSTRRQR 12
Db	4 RKLMLKSTRRQR 15
	RESULT 8
ID	ADS17621
ID	ADS17621 standard; peptide; 27 AA.
XX	
AC	ADS17621;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Amino acid sequence of protein transduction domain (PTD) peptide #4.
XX	
KW	protein transduction domain; PTD; PTD-cargo moiety complex;
KW	cell immortalisation; cell viability; internalising peptide;
KW	cell transport.
XX	
OS	Synthetic.
XX	
PN	WO2004078933-A2.
XX	
PD	16-SEP-2004.
XX	
PR	04-MAR-2004; 2004WO-US006445.
PR	03-MAR-2004; 2004US-00790768.
XX	
PA	(BIOW-) BIOWHITTAKER TECHNOLOGIES INC.
PA	
PA	Karas M;
XX	
DR	WPI; 2004-653708/63.
XX	
PT	New isolated and purified polypeptide with a protein transduction domain, PT useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
XX	
PS	Disclosure; SEQ ID NO 5; 60pp; English.
XX	
CC	The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal Lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker and 2 nuclear localisation signals.
CC	
XX	
DR	Sequence 27 AA;
XX	
PT	Query Match 100.0%; Score 58; DB 8; Length 27;
PT	Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
XX	
PS	Example 10; SEQ ID NO 19; 60pp; English.
XX	
CC	The specification describes Peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal Lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.
CC	
XX	
SQ	Sequence 21 AA;
	Query Match 100.0%; Score 58; DB 8; Length 21;
	Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RKLMLKSTRRQR 12
Db	4 RKLMLKSTRRQR 15
	RESULT 9
ID	ADS17634
ID	ADS17634 standard; peptide; 19 AA.
XX	
AC	ADS17634;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Amino acid sequence of a PTD designated peptide 13.
XX	
KW	protein transduction domain; PTD; PTD-cargo moiety complex;
KW	cell immortalisation; cell viability; internalising peptide;
KW	cell transport.
XX	

OS Synthetic.
 XX
 FH
 FT Modified-site 1 location/Qualifiers
 FT /note= "biotin attached"
 XX
 PN WO2004078933-A2.
 XX
 PD 16-SEP-2004.
 XX
 PR 04-MAR-2004; 2004WO-US006445.
 XX
 PR 04-MAR-2003; 2003US-0451243P.
 XX
 PR 03-MAR-2004; 2004US-00790768.
 XX
 PA (BIOW-) BIOMHITTAKER TECHNOLOGIES INC.
 XX
 PT Karas M;
 XX
 DR WPI; 2004-653708/63.
 XX
 PT New isolated and purified polypeptide with a protein transduction domain, useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
 XX
 PS Example 10; SEQ ID NO 22; 60pp; English.
 XX
 CC The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.
 CC
 CC
 XX Sequence 19 AA;
 XX
 Query Match 82.8%; Score 48; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 MLKSTRRQR 12
 Db 10 MLKSTRRQR 19
 RESULT 10
 ADS17638
 ID ADS17638 Standard; peptide; 25 AA.
 XX
 AC ADS17638;
 XX
 DT 02-DEC-2004 (first entry)
 DB Amino acid sequence of a PTD designated peptide 17.
 XX
 KW protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide; cell transport.
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 location/Qualifiers
 FT /note= "biotin attached"
 XX
 PN WO2004078933-A2.
 XX
 PD 16-SEP-2004.
 XX
 PR 04-MAR-2004; 2004WO-US006445.
 XX
 PR 04-MAR-2003; 2003US-0451243P.
 PR 03-MAR-2004; 2004US-00790768.
 XX
 PA (BIOW-) BIOMHITTAKER TECHNOLOGIES INC.
 XX
 PT Karas M;
 XX
 DR WPI; 2004-653708/63.
 XX
 PT New isolated and purified polypeptide with a protein transduction domain,

PT	useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.	CC
XX	Example 10; SEQ ID NO 21; 60pp; English.	CC
CC	The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. AU17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.	CC
CC	Sequence 25 AA;	CC
SQ	Query Match 82.8%; Score 48; DB 8; Length 25; Best Local Similarity 100.0%; Pred. No. 0.58; Mismatches 0; Indels 0; Gaps 0; Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0; QY 3 MLKSTRRQR 12 Db 10 MLKSTRRQR 19	CC
RESULT 12		CC
AAU50525		CC
ID AAU50525 standard; protein; 63 AA.		CC
AC XX		CC
DE XX		CC
XX AAU50525;		CC
DT 13-FEB-2002 (first entry)		CC
DE Propionibacterium acnes immunogenic protein #11421.		CC
KW SAPRO syndrome; bryonitis; acne; pustulosis; hypertosis; osteomyelitis; uvitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.		CC
KW XX		CC
OS OS Propionibacterium acnes.		CC
XX PN WO200181581-A2.		CC
PD XX 01-NOV-2001.		CC
XX PF 20-APR-2001; 2001WO-US012865.		CC
PR XX 21-APR-2000; 2000US-019947P.		CC
PR XX 02-TUN-2000; 2000US-020841P.		CC
PR XX 07-JUL-2000; 2000US-0216747P.		CC
PA (CORT-) CORIXA CORP.		CC
XX PI Skeik YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;		CC
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;		CC
DR DR WPI; 2001-616774/71.		CC
DR DR N-PSDB; AAS5949.		CC
PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.		CC
PT Example 1; SEQ ID NO 11720; 1069pp; English.		CC
XX Sequences AU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPRO syndrome (bryonitis, acne, pubulosis, hypertosis and osteomyelitis); uvitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes protein. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pct_sequences	CC	
SQ Sequence 63 AA;		CC
Query Match 74.1%; Score 43; DB 4; Length 63; Best Local Similarity 75.0%; Pred. No. 9.4; Mismatches 1; Indels 0; Gaps 0; Matches 9; Conservative 1; MisMatches 2; Indels 0; Gaps 0; QY 1 RKLMLKSTRQR 12 Db 48 RKLULKKTRIOR 59		CC
RESULT 13		CC
ABM47044		CC
ID ABM47044 standard; protein; 63 AA.		CC
AC XX		CC
DE ABM47044;		CC
XX DT 20-OCT-2003 (first entry)		CC
DE Propionibacterium acnes predicted ORF-encoded polypeptide #11720.		CC
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.		CC
KW OS Propionibacterium acnes.		CC
PN PN WO2003033515-A1.		CC
XX PD 24-APR-2003.		CC
XX PP 11-OCT-2002; 2002WO-US032727.		CC
XX PR 15-OCT-2001; 2001US-00978825.		CC
XX PA (CORT-) CORIXA CORP.		CC
XX PI Mitcham JL, Skeik YAW, Persing DH, Bhatia A, Maisonneuve JL, Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D, Barth B, Valliere-Douglas J;		CC
XX DR WPI; 2003-38179/36.		CC
DR DR N-PSDB; ACP64478.		CC
XX Example 1; SEQ ID NO 11720; 1481pp; English.		CC
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.		CC
XX PS Example 1; SEQ ID NO 11720; 1481pp; English.		CC
CC The invention relates to an isolated polynucleotide (ACP64475-ACF64731) encoding a Propionibacterium acnes protein. The invention also relates to CC additional polypeptides encoded by the polynucleotides (ABM3624-ABM64336) and to CC immunogenic fragments of P. acnes polypeptides. The invention CC encompasses expression vectors and host cells comprising a CC polynucleotide of the invention; antibodies against polypeptides of the CC invention; fusion proteins comprising a polypeptide of the invention; a CC method for stimulating an immune response specific for a P. acnes CC polypeptide and an isolated T cell population comprising T cells prepared	CC	

CC via this method; a vaccine composition (comprising *P. acnes* polypeptides, CC polymucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit CC for detecting or determining the presence or absence of *P. acnes* in a patient; and a method for inhibiting the development of *P. acnes* in a patient. The *P. acnes* polypeptides, polymucleotides, antibodies, fusion CC proteins, T cell populations or antigen-presenting cells that express the CC polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a *P. acnes* protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridization. The vaccine composition is useful for the stimulation of an immune response against *P. acnes*, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the *P. acnes* polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 63 AA;

Query Match 74.1%; Score 43; DB 6; Length 63;

Best Local Similarity 75.0%; Pred. No. 9.4; Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKMVKSTRRQR 12
DB 48 RKLJKKTR-IQR 59

RESULT 14

ADU70413 Best Local Similarity 75.0%; Pred. No. 9.4; Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

ID ADU70413 Standard; protein; 247 AA.

XX AC ADU70413;

XX DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2219.

XX KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy; ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic;

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US10870.

XX PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX PA (MTO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RBS.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BM, Taylor SW, Glenn GM;

PI Warnock DE;

XX DR WPI; 2003-845369/78.

PS Claim 1; SEQ ID NO 2219; 180PP; English.
XX This invention relates to novel mitochondrial targets that can be used CC for therapeutic intervention in treating a disease associated with CC altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are CC useful for drug screening assays, as well as therapeutic targets. The CC present invention describes a method for identifying such proteins that CC can be used in the treatment of various diseases associated with altered CC mitochondrial function including diabetes mellitus, Huntington's disease, CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these CC compositions have neuroprotective, nontropic, antidiabetic, CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and CC cytostatic activities. This polypeptide sequence is a human heart CC mitochondrial protein of the invention.

XX SQ Sequence 247 AA;

Query Match 74.1%; Score 43; DB 7; Length 247;

Best Local Similarity 81.8%; Pred. No. 34; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKMVKSTRRQR 11
DB 130 RKSILKSTRRR 140

RESULT 15

AAG90210 Best Local Similarity 81.8%; Pred. No. 34; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ID AAG90210 Standard; protein; 33 AA.

XX AC AAG90210;

XX DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 3964.

XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KW organic acid synthesis.

XX OS Corynebacterium glutamicum.

XX PN EP108790-A2.

XX PD 20-JUN-2001.

XX PF 18-DEC-2000; 2000EP-0012768B.

XX PR 16-DEC-1999; 98JP-0037744.

PR 07-APR-2000; 2000JP-00159152.

PR 03-AUG-2000; 2000JP-0028098B.

XX PA (KJOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX DR WPI; 2001-376931-40.

DR N-PSDB; AAH65429.

XX PS Claim 17; SEQ ID NO 3964; 246PP + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium *Corynebacterium glutamicum*. These sequences are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from

CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-Lysine. The present sequence is a protein described in the
CC exemplification of the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the European Patent Office
XX

Sequence 33 AA;

Query Match 72.4%; Score 42; DB 4; Length 33;
Best Local Similarity 75.0%; Pred. No. 7.5;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRQR 12
Db 18 RKLMLRTRVQR 29

Search completed: February 4, 2006, 03:36:12
Job time : 253.944 secs

GenCore version 5.1.7														
Run on:	February 4, 2006, 03:36:41 : Search time 22.6667 seconds (without alignments) 50.938 Million cell updates/sec													
Title:	OM protein - protein search, using sw model													
Perfect score:	US-10-790-768A-1													
Sequence:	1 RKKMKSTRRQRR 12													
Scoring table:	BLOSUM62													
Searched:	Gapop 10.0 , Gapext 0.5 283416 seqs, 96216763 residues													
Total number of hits satisfying chosen parameter:	283416													
Minimum DB seq length:	0													
Maximum DB seq length:	200000000													
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries													
Database :	PIR 80: 1: Pirl: 2: Pir2: 3: Pir3: 4: Pir4: SUMMARIES													
Result No.	Score	Query Length	DB ID	Description										
1	42	72.4	32	2 T36275										
2	39	67.2	33	2 A87213	hypothetical prote									
3	39	67.2	258	2 T24499	hypothetical prote									
4	38	65.5	2	A81979	ABC transporter AT									
5	37	63.8	651	2 T10219	protein kinase hom									
6	36	62.1	69	2 S39424	procamine PI - Aub									
7	36	62.1	89	2 T29955	hypothetical prote									
8	35	60.3	110	2 S15153	hypothetical prote									
9	35	60.3	308	2 A85904	probable transcript									
10	35	60.3	308	2 H65035	hypothetical prote									
11	35	60.3	308	2 C91059	probable transcript									
12	35	60.3	829	2 A40194	RNA-directed RNA p									
13	35	60.3	1017	2 T31354	probable potassium									
14	35	60.3	1020	2 E86165	F15K9.2 protein -									
15	35	60.3	1701	2 T09127	probable erythrocy									
16	34	58.6	281	2 G77680	hypothetical prote									
17	34	58.6	317	2 T39736	hypothetical prote									
18	34	58.6	327	2 E91181	dipeptide transpor									
19	34	58.6	341	2 E61404	dipeptide transpor									
20	34	58.6	327	2 A86028	dipeptide transpor									
21	34	58.6	367	2 T44887	copalamin biosynth									
22	34	58.6	386	2 T44887	hypothetical prote									
23	34	58.6	500	2 T19525	hypothetical prote									
24	34	58.6	647	2 E64170	ABC-type transport									
25	34	58.6	2793	2 B90784	hypothetical prote									
26	34	58.6	2806	2 D85944	hypothetical prote									
27	33	56.9	47	2 S22828	protamine - killer									
28	33	56.9	57	2 T36555	50S ribosomal prot									
29	33	56.9	58	2 S10755	protamine ST2b - h									
ALIGNMENTS														
RESULT 1														
T36275														
hypothetical protein SCB68.25c - Streptomyces coelicolor														
C;Species:	Streptomyces coelicolor													
C;Accession:	T36275													
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.	submitted to the EMBL Data Library, June 1999													
A;Reference number:	221576													
A;Accession:	T36275													
A;Status:	preliminary; translated from GB/EMBL/DDJB													
A;Molecule type:	DNA													
A;Cross-references:	UNIPROT:Q9WX07; UNIPARC:UPI00000DB13D; EMBL:AL079345; PIDN:CA45361; C;Genetics:													
A;Gene:	SCB68.25C													
Query	Match	72.4%; Score 42; DB 2; Length 32;												
Best Local	Similarity	75.0%; Pred. No. 0.63; 1; Mismatches												
Matches	9;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;					
RESULT 2														
Qy	1	RKKMKSTRRQRR	12											
Db	18	RKKMKSTRRQRR	29											
hypothetical protein MLU2428A [imported] - Mycobacterium leprae														
C;Species:	Mycobacterium leprae													
C;Accession:	T36275													
C;Change:	20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004													
R;Cole, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hedges, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, M.A.; Rutherford, K.M.	Nature 409, 100-101, 2001													
A;Authors:	Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Stables, A.; Reference number: A86909; MUID:21128732; PMID:11234002													
A;Accession:	A86909													
A;Status:	preliminary													
A;Molecule type:	DNA													
A;Residues:	1-33 <STO>													
C;Genetics:	C;Gene: ML2428A													
Query	Match	67.2%; Score 39; DB 2; Length 33;												
Best Local	Similarity	66.7%; Pred. No. 2.2; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;												
Matches	8;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;					

RESULT 3

T24499 hypothetical protein T05A6.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T24499 submitted to the EMBL Data Library, August 1995
 A;Reference number: 219899
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-258 <WIL>
 A;Experimental source: clone T05A6
 C;Genetics:
 C;Gene: CESP:T05A6.2
 A;Map position: 2
 A;Introns: 25/3; 134/2; 157/1; 211/2

Query Match 67.2%; Score 39; DB 2; Length 258;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQR 12
 Db 240 KKKMTTSSRSR 251

RESULT 4

AE1779 ABC transporter ATP-binding protein alr1384 [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 C;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
 C;Accession: AE1779
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AE1779
 A;Molecule type: DNA
 A;Residues: 1-61 <KOR>
 A;Cross-references: UNIPROT:QBVX34; UNIPARC:UPI00000CE09F; GB:BA000019; PIDN:BBT3341.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 C;Gene: alr1384

Query Match 65.5%; Score 38; DB 2; Length 361;
 Best Local Similarity 72.7%; Pred. No. 29;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQR 11
 Db 122 RRMQKSRRQR 132

RESULT 5

T10219 protein kinase homolog T00C3.60 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10219
 R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
 Submitted to the Protein Sequence Database, June 1999
 A;Reference number: 216897

A;Accession: T10219
 A;Molecule type: DNA
 A;Residues: 1-651 <BEV>
 A;Cross-references: UNIPROT:Q9S9J8; UNIPARC:UPI00000489E8; EMBL:AL079350; GSPDB:GN00062;
 A;Experimental source: cultivar Columbia; BAC clone T30C3
 C;Genetics:
 C;Gene: ATSP:T30C3.60
 A;Map position: 4

Query Match 63.8%; Score 37; DB 2; Length 651;
 Best Local Similarity 77.8%; Pred. No. 76;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKSTRRQR 12
 Db 643 LKTRKRQR 651

RESULT 6

S39424 protamine P1 - Australian echidna
 C;Species: *Tachyglossus aculeatus* (Australian echidna)
 C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C;Accession: S39424
 R;Retief, J.D.; Winkfein, R.J.; Dixon, G.H.
 A;Title: Evolution of the monotremes. The sequences of the protamine P1 genes of platypu
 A;Reference number: S39424; MUID:94094837; PMID:826934
 A;Accession: S39424
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-69 <RET>
 A;Cross-references: UNIPROT:P35311; UNIPARC:UPI000016C71A; EMBL:Z26848; NID:5407103; PID:
 C;Genetics:
 A;Introns: 5/1
 C;Keywords: sperm histone
 C;Superfamily: DNA binding

Query Match 60.1%; Score 36; DB 2; Length 69;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQR 12
 Db 54 RRSNRSSRRRR 65

RESULT 7

T29995 hypothetical protein C43H6.8 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29995
 R;Le, T.T.
 Submitted to the EMBL Data Library, March 1996
 A;Description: The sequence of *C. elegans* cosmid C43H6.
 A;Reference number: 22017
 A;Accession: T29995
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-89 <LET>
 A;Cross-references: UNIPROT:Q18590; UNIPARC:UPI0000077B96; EMBL:U51999; PIDN:AAA96089.1;
 A;Experimental source: strain Bristol N2; Clone C43H6
 C;Genetics:
 C;Gene: CESP:C43H6.8
 A;Map position: X
 A;Introns: 42/2

Query Match 62.1%; Score 36; DB 2; Length 89;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQR 12

Db 16 RKLISKERRICKR 27
RESULT 8
 hypothetical protein 110 - phage Pf1
 C;Species: phage Pf1
 C;Date: 18-Feb-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
 C;Accession: S15153; S08824
 R;HILL, D.F.; Short, N.J.; Perham, R.N.; Petersen, G.B.
 J; Mol. Biol. 218, 349-364, 1991.
 A;Title: DNA sequence of the filamentous bacteriophage Pf1.
 A;Reference number: S15140; MUID:91186399; PMID:2010913
 A;Molecule type: DNA
 A;Residues: 1-110 <JMO>
 A;Cross-references: UNIPROT:P25132; UNIPARC:UPI0001384CE; EMBL:X52107; NID:G14829; PIDN:
 A;Experimental source: ATCC 25102-B1
Query Match 60.3%; Score 35; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 33; Mismatches 8; Conservative 0; Indels 4; Gaps 0;
 Matches 7; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKLISKERRICKR 12
 Db 68 RQALPSTRQER 79
RESULT 9
 A65904
 probable transcription regulator LYSR-type YfIE [imported] - Escherichia coli (strain O1
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C;Accession: A85904
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mai, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamouidis, K.; Apodaca, Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: A85904
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <STO>
 A;Cross-references: UNIPROT:Q8X5A8; UNIPARC:UPI00000D0C85; GB:AE005174; NID:912516998; F
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: yfIE
 C;Superfamily: HTH-type transcriptional regulator, LysR family, MetR type
Query Match 60.3%; Score 35; DB 2; Length 308;
 Best Local Similarity 58.3%; Pred. No. 86; Mismatches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKLISKERRICKR 12
 Db 213 RQIFESTLRQRR 224
RESULT 10
 H65035
 hypothetical protein srmB-ung intergenic region - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
 C;Accession: H65035
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A;Rose, D.J.; Mau, B.; Shao, Y.; Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: H65035
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-308 <BLAT>
 A;Cross-references: UNIPARC:UPI000168148; GB:AB000344; GB:U00096; NID:G1788927; PIDN:AA
 A;Experimental source: strain K-12, substrain McI655
 C;Genetics:
 A;Gene: yfIE
 C;Superfamily: HTH-type transcriptional regulator, LysR family, MetR type
Query Match 60.3%; Score 35; DB 2; Length 308;
 Best Local Similarity 58.3%; Pred. No. 86; Mismatches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKLISKERRICKR 12
 Db 213 RQIFESTLRQRR 224
RESULT 11
 C91059
 probable transcription regulator LYSR-type [imported] - Escherichia coli (strain O157:H7)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
 C;Accession: C91059
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gabbara, N.; Yabunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
 A;Reference number: A99629; MUID:21156231; PMID:12158796
 A;Accession: C91059
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <HAY>
 A;Cross-references: UNIPROT:Q8X5A8; UNIPARC:UPI00000D0C85; GB:BA000007; PIDN:BAB36866.1;
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: EC03443
 C;Superfamily: HTH-type transcriptional regulator, LysR family, MetR type
Query Match 60.3%; Score 35; DB 2; Length 308;
 Best Local Similarity 58.3%; Pred. No. 86; Mismatches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKLISKERRICKR 12
 Db 213 RQIFESTLRQRR 224
RESULT 12
 A40894
 RNA-directed RNA polymerase (EC 2.7.7.48) - yeast (Saccharomyces cerevisiae) RNA replicon
 C;Species: Saccharomyces cerevisiae
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Oct-2004
 C;Accession: A40894; A40855
 R;Rodriguez-Cousino, N.; Esteban, L.M.; Esteban, R.; J. Biol. Chem. 266, 12772-12778, 1991.
 A;Title: Molecular cloning and characterization of W double-stranded RNA, a linear molecule
 A;Reference number: A40894; MUID:91286317; PMID:2061340
 A;Accession: A40894
 A;Molecule type: genomic RNA
 A;Residues: 1-829 <ROD>
 A;Cross-references: UNIPROT:P25328; UNIPARC:UPI000134B87; GB:M63893; NID:G4090991; PIDN:
 R;Matsumoto, Y.; Wickner, R.B.; J. Biol. Chem. 266, 12779-12783, 1991
 A;Title: Yeast 20 S RNA replicon. Replication intermediates and encoded putative RNA polymerase
 A;Reference number: A40895; MUID:91286318; PMID:1648104
 A;Accession: A40895
 A;Molecule type: genomic RNA
 A;Residues: 1-825, 'V' <MAT>
 A;Cross-references: UNIPARC:UPI00005BD1; GB:M64034; NID:G335015; PID:G555371
 C;Superfamily: RNA-directed RNA polymerase in W dsRNA
 C;Keywords: nucleotidytransferase

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RKLKMKSTRQRR 12
 Db 320 RLFFKGRLRR 331

RESULT 13

T31354 probable potassium channel elk chain 1 - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Accession: T31354
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 R;England, B.; Neu, A.; Ludwig, J.; Roepke, J.; Pongb, O.
 A;Description: Identification of three rat potassium channel genes homologous to *D. mela*
 A;Reference number: Z20983
 A;Accession: T31354
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1701 <KAP>
 A;Cross-references: UNIPROT:Q9R1T9; UNIPARC:UPI0000170A85; EMBL:AJ007628; NID:e1329997;
 A;Experimental source: cortex
 C;Genetics:
 A;Gene: slk1
 C;Keywords: potassium channel

Query Match 60.3%; Score 35; DB 2; Length 1017;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 LKSTRQR 12
 Db 166 LRSTRQRN 174

RESULT 14

E86165 F1K9.2 protein - *Arabidopsis thaliana* (mouse-ear cress)
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: E86165
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creeley, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creeley, T.H.; Dewar, K.; anson, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hobson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luces, J.S.; Maiti, R.; Mazziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: E86165
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9ZVT9; UNIPARC:UPI000017CB8B; GB:AE005172; NID:93850588; PI
 C;Genetics:
 A;Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 1020;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 LKSTRQR 12
 Db 978 LRSTRQR 986

RESULT 15

T09127 probable erythrocyte-binding protein MABBL - *Plasmodium yoelii*

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 4, 2006, 03:26:53 ; Search time 135.556 Seconds
(without alignments)
62.457 Million cell updates/sec

Title: US-10-790-768A-1

Perfect score: 58

Sequence: 1 RKLMLKSTRRORR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74.1	32	2 QANDY7_9MICC	Qandy7 arthropbacte
2	74.1	33	2 06AAZ0_PROAC	06aaZ0 propionibac
3	72.4	32	2 09WK07_STREOC	09wk07 streptomyce
4	72.4	33	2 04JSKX_CORTK	04jskx corticbacte
5	72.4	33	2 08PSGO_COBEP	08psgo corynebacte
6	72.4	33	2 08NT95_COGBU	08nt95 corynebacte
7	69.0	125	2 08RHB6_ECOL6	08rhb6 escherichia
8	69.0	589	2 09ZTLL_CYACCA	09ztll cyanidium c
9	69.0	646	2 065UB3_MANS1	065ub3 marinheimia
10	67.2	33	1 Y2WQN2_MYCIB	poasedo mycobacteri
11	67.2	33	1 Y500A_NYCTU	poascg mycobacteri
12	67.2	69	1 R8211_TREBDE	R8211 treponema d
13	67.2	75	2 06NJK5_CORDT	06njk5 cornebacte
14	67.2	258	2 022198_CAEEL	022198 caenorhabdi
15	67.2	259	2 09U6R5_CABEE	09u6r5 caenorhabdi
16	67.2	279	2 09AUVE_ORYSA	09auv5 oryza sativ
17	67.2	383	2 04WQN2_ASFRU	04wqn2 aspergillus
18	67.2	424	2 05WM29_ORYSA	05wm29 oryza sativ
19	67.2	674	2 07SBH2_NEUGER	07sbh2 neurospora
20	65.5	228	2 07ZWE7_BRARE	07zwe7 brachythamn
21	65.5	361	2 08YX34_ANASD	08yx34 anaebaena sp
22	65.5	655	2 0522YI_WAGBR	0522yi magnaporthe
23	65.5	1830	2 04SJA7_TETNG	04sja7 tetradacon
24	65.5	417	2 058D2_9TRYP	058d2 trypanosoma
25	63.8	196	2 04RHP2_TETNG	04rhp2 tetradacon
26	63.8	282	2 08LMH0_ORYSA	08lmh0 oryza sativ
27	63.8	386	2 08SL62_ORYSA	08sl62 oryza sativ
28	63.8	402	1 KLF12_HUMAN	09y434 homo sapien
29	63.8	402	1 KLF12_MOUSE	035738 mus musculus
30	63.8	402	2 Q8WV13_HUMAN	08ww13 homo sapien
31	63.8	402	2 Q5VZM7_HUMAN	Q5vzm7 homo sapien

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74.1	32	2 QANDY7_9MICC	Qandy7 arthropbacte
2	74.1	33	2 06AAZ0_PROAC	06aaZ0 propionibac
3	72.4	32	2 09WK07_STREOC	09wk07 streptomyce
4	72.4	33	2 04JSKX_CORTK	04jskx corticbacte
5	72.4	33	2 08PSGO_COBEP	08psgo corynebacte
6	72.4	33	2 08NT95_COGBU	08nt95 corynebacte
7	69.0	125	2 08RHB6_ECOL6	08rhb6 escherichia
8	69.0	589	2 09ZTLL_CYACCA	09ztll cyanidium c
9	69.0	646	2 065UB3_MANS1	065ub3 marinheimia
10	67.2	33	1 Y2WQN2_MYCIB	poasedo mycobacteri
11	67.2	33	1 Y500A_NYCTU	poascg mycobacteri
12	67.2	69	1 R8211_TREBDE	R8211 treponema d
13	67.2	75	2 06NJK5_CORDT	06njk5 cornebacte
14	67.2	258	2 022198_CAEEL	022198 caenorhabdi
15	67.2	259	2 09U6R5_CABEE	09u6r5 caenorhabdi
16	67.2	279	2 09AUVE_ORYSA	09auv5 oryza sativ
17	67.2	383	2 04WQN2_ASFRU	04wqn2 aspergillus
18	67.2	424	2 05WM29_ORYSA	05wm29 oryza sativ
19	67.2	674	2 07SBH2_NEUGER	07sbh2 neurospora
20	65.5	228	2 07ZWE7_BRARE	07zwe7 brachythamn
21	65.5	361	2 08YX34_ANASD	08yx34 anaebaena sp
22	65.5	655	2 0522YI_WAGBR	0522yi magnaporthe
23	65.5	1830	2 04SJA7_TETNG	04sja7 tetradacon
24	65.5	417	2 058D2_9TRYP	058d2 trypanosoma
25	63.8	196	2 04RHP2_TETNG	04rhp2 tetradacon
26	63.8	282	2 08LMH0_ORYSA	08lmh0 oryza sativ
27	63.8	386	2 08SL62_ORYSA	08sl62 oryza sativ
28	63.8	402	1 KLF12_HUMAN	09y434 homo sapien
29	63.8	402	1 KLF12_MOUSE	035738 mus musculus
30	63.8	402	2 Q8WV13_HUMAN	08ww13 homo sapien
31	63.8	402	2 Q5VZM7_HUMAN	Q5vzm7 homo sapien

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74.1	32	2 QANDY7_9MICC	Qandy7 arthropbacte
2	74.1	33	2 06AAZ0_PROAC	06aaZ0 propionibac
3	72.4	32	2 09WK07_STREOC	09wk07 streptomyce
4	72.4	33	2 04JSKX_CORTK	04jskx corticbacte
5	72.4	33	2 08PSGO_COBEP	08psgo corynebacte
6	72.4	33	2 08NT95_COGBU	08nt95 corynebacte
7	69.0	125	2 08RHB6_ECOL6	08rhb6 escherichia
8	69.0	589	2 09ZTLL_CYACCA	09ztll cyanidium c
9	69.0	646	2 065UB3_MANS1	065ub3 marinheimia
10	67.2	33	1 Y2WQN2_MYCIB	poasedo mycobacteri
11	67.2	33	1 Y500A_NYCTU	poascg mycobacteri
12	67.2	69	1 R8211_TREBDE	R8211 treponema d
13	67.2	75	2 06NJK5_CORDT	06njk5 cornebacte
14	67.2	258	2 022198_CAEEL	022198 caenorhabdi
15	67.2	259	2 09U6R5_CABEE	09u6r5 caenorhabdi
16	67.2	279	2 09AUVE_ORYSA	09auv5 oryza sativ
17	67.2	383	2 04WQN2_ASFRU	04wqn2 aspergillus
18	67.2	424	2 05WM29_ORYSA	05wm29 oryza sativ
19	67.2	674	2 07SBH2_NEUGER	07sbh2 neurospora
20	65.5	228	2 07ZWE7_BRARE	07zwe7 brachythamn
21	65.5	361	2 08YX34_ANASD	08yx34 anaebaena sp
22	65.5	655	2 0522YI_WAGBR	0522yi magnaporthe
23	65.5	1830	2 04SJA7_TETNG	04sja7 tetradacon
24	65.5	417	2 058D2_9TRYP	058d2 trypanosoma
25	63.8	196	2 04RHP2_TETNG	04rhp2 tetradacon
26	63.8	282	2 08LMH0_ORYSA	08lmh0 oryza sativ
27	63.8	386	2 08SL62_ORYSA	08sl62 oryza sativ
28	63.8	402	1 KLF12_HUMAN	09y434 homo sapien
29	63.8	402	1 KLF12_MOUSE	035738 mus musculus
30	63.8	402	2 Q8WV13_HUMAN	08ww13 homo sapien
31	63.8	402	2 Q5VZM7_HUMAN	Q5vzm7 homo sapien

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74.1	32	2 QANDY7_9MICC	Qandy7 arthropbacte
2	74.1	33	2 06AAZ0_PROAC	06aaZ0 propionibac
3	72.4	32	2 09WK07_STREOC	09wk07 streptomyce
4	72.4	33	2 04JSKX_CORTK	04jskx corticbacte
5	72.4	33	2 08PSGO_COBEP	08psgo corynebacte
6	72.4	33	2 08NT95_COGBU	08nt95 corynebacte
7	69.0	125	2 08RHB6_ECOL6	08rhb6 escherichia
8	69.0	589	2 09ZTLL_CYACCA	09ztll cyanidium c
9	69.0	646	2 065UB3_MANS1	065ub3 marinheimia
10	67.2	33	1 Y2WQN2_MYCIB	poasedo mycobacteri
11	67.2	33	1 Y500A_NYCTU	poascg mycobacteri
12	67.2	69	1 R8211_TREBDE	R8211 treponema d
13	67.2	75	2 06NJK5_CORDT	06njk5 cornebacte
14	67.2	258	2 022198_CAEEL	022198 caenorhabdi
15	67.2	259	2 09U6R5_CABEE	09u6r5 caenorhabdi
16	67.2	279	2 09AUVE_ORYSA	09auv5 oryza sativ
17	67.2	383	2 04WQN2_ASFRU	04wqn2 aspergillus
18	67.2	424	2 05WM29_ORYSA	05wm29 oryza sativ
19	67.2	674	2 07SBH2_NEUGER	07sbh2 neurospora
20	65.5	228	2 07ZWE7_BRARE	07zwe7 brachythamn
21	65.5	361	2 08YX34_ANASD	08yx34 anaebaena sp
22	65.5	655	2 0522YI_WAGBR	0522yi magnaporthe
23	65.5	1830	2 04SJA7_TETNG	04sja7 tetradacon
24	65.5	417	2 058D2_9TRYP	058d2 trypanosoma
25	63.8	196	2 04RHP2_TETNG	04rhp2 tetradacon
26	63.8	282	2 08LMH0_ORYSA	08lmh0 oryza sativ
27	63.8	386	2 08SL62_ORYSA	08sl62 oryza sativ
28	63.8	402	1 KLF12_HUMAN	09y434 homo sapien
29	63.8	402	1 KLF12_MOUSE	035738 mus musculus
30	63.8	402	2 Q8WV13_HUMAN	08ww13 homo sapien
31	63.8	402	2 Q5VZM7_HUMAN	Q5vzm7 homo sapien

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74.1	32	2 QANDY7_9MICC	Qandy7 arthropbacte
2	74.1	33	2 06AAZ0_PROAC	06aaZ0 propionibac
3	72.4	32	2	

RESULT 6

ID Q8NT95_CORGL
ID Q8NT95_CORGL PRELIMINARY;
AC 08NT95; 06M7V0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 03-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein Cgl0413;
GN OrderobacteriumNames=Cgl0413, cgl0494;
OS Corynebacterium glutamicum (Brevibacterium flavidum)
Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OC OX NCBI_TaxID=1718;
RN [1] _
RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RC NUCLEOTIDE SEQUENCE;
RA Nucleotide sequence of Corynebacterium glutamicum ATCC 13032.;"
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE;
RA STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=22830012; PubMed=12988626; DOI=10.1016/S0168-1656(03)00154-8;
RA Kallnowski J., Batte B., Barrels D., Bischoff N., Bott M.,
RA Buckowski A., Dubach N., Eggeling L., Eikmanns B.J., Gaigalat L.,
RA Goessmann A., Hartmann M., Hutchmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moekel B., Pfefferle W., Puebler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegraebe I.,
RA Tauch A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
and its impact on the production of L-aspartate-derived amino acids
and vitamins.";
RT J. Biotechnol. 104:5-25(2003).
DR EMBL; BX927149; CAR19130.1; -; Genomic_DNA.
DR EMBL; BX927149; CAR19130.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 33 AA; 4163 MW;

Query Match Best local Similarity 72.4%; Score 42; DB 2; Length 33;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKMURTRRORR 12
Db 18 RKMURTRRORR 29

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=217992;

RN [1]
RP NUCLEOTIDE SEQUENCE;
RC STRAIN=O:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=2288234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackert J., Stroud D.,
RA Mayhew G.J., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RT PROC. NATL. ACAD. SCI. U.S.A. 99:17020-17024 (2002).

RESULT 7

ID Q8FBG_ECOL6
ID Q8FBG_ECOL6 PRELIMINARY;
AC 08FBG;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative acid shock protein.
GN OrderobacterNames=c1989;
OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=217992;

RN [1]
RP NUCLEOTIDE SEQUENCE;
RC STRAIN=O:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=2288234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackert J., Stroud D.,
RA Mayhew G.J., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RT PROC. NATL. ACAD. SCI. U.S.A. 99:17020-17024 (2002).

RESULT 8

ID Q9ZTLI_CVACA
ID Q9ZTLI_CVACA PRELIMINARY;
AC Q9ZTLI;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DR RNA polymerase sigma factor.
GN Name=rpoD2;
OS Cyanidium caldarium.
OC Eukarya; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;

RP NUCLEOTIDE SEQUENCE;
RA STRAIN=111-D-2;
RC STRAIN=111-D-2;
RA Troxler R.F., Tan S., Liu B.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050634; AAC02575.1; -; Genomic_DNA.
RN [1]
RP NUCLEOTIDE SEQUENCE;
RA GO; GO:0016987; sigma factor activity; IEA.
DR GO; GO:0003700; transcription factor activity, DNA-dependent; IEA.
DR GO; GO:0006312; transcription initiation; IEA.
DR HSSP; Q9W78; 1IW7.
DR InterPro; IPR005727; Sigma70_r1.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR007624; Sigma70_r3.
DR InterPro; IPR007630; Sigma70_r4.
DR InterPro; IPR000943; Sigma70.
DR Pfam; PF00140; Sigma70_r1_2; 1.
DR Pfam; PF04542; Sigma70_r2; 1.
DR Pfam; PF04539; Sigma70_r3; 1.
DR Pfam; PF04545; Sigma70_r4; 1.
DR PRINTS; PR00046; SIGMA70PCT.
DR PROSITE; PS00715; SIGMA70_1; UNKNOWN_1.
DR PROSITE; PS00716; SIGMA70_2; 1.
SQ SEQUENCE 589 AA; 69127 MW; 751E2631DCB9814F CRC64;

Query Match Best local Similarity 69.0%; Score 40; DB 2; Length 589;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKMURTRRORR 12
Db 92 RQVVKSSRKRR 103

RESULT 9

ID Q65UB3_MANSM
ID Q65UB3_MANSM PRELIMINARY;
AC Q65UB3;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DR Up protein.
GN Name=up; OrderobacterName=MS0840;
OS Mannheimia succiniciproducens (strain MBE155E)
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=22198;

RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	PubMed=537867; DOI=10.1038/nbt1010;
RA	Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K., Kim H.J., Jeong H., Hur C.G., Kim J.J.; "The genome sequence of the cappnophilic rumen bacterium Mannheimia succiniciproducens,"; Nat. Biotechnol. 22:1275-1281 (2004).
RT	"-- SIMILARITY: Belongs to the ABC transporter family.
RL	Nat. Biotechnol. 22:1275-1281 (2004).
CC	--
DR	EMBL; AR016827; AU3747.1; -, Genomic_DNA.
DR	GO; GO:0005524; FATP binding; IEA.
DR	GO; GO:0001687; FATPase activity; IEA.
DR	GO; GO:000166; F-nucleotide binding; IEA.
DR	InterPro; IPR003593; AAA ATPase.
DR	pfam; PF00055; ABC_tran_2.
DR	PRODOM; PD00006; ABC transporter; 1.
DR	SMART; SM00382; AAA_2.
DR	PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_2.
DR	PROSITE; PS50093; ABC_TRANSPORTER_2; 2.
KW	ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ	SEQUENCE 646 AA; 73203 MW; 1C1B0A365CE6BB6 CRC64;
Query Match	69.0%; Score 40; DB 2; Length 646;
Best Local Similarity	72.7%; Pred. No. 87;
Matches	8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY	1 RKLRRRTVQRR 12
Db	18 RKLRRRTVQRR 29
RESULT 11	
ID	Y500A MYCTU STANDARD; PRT; 33 AA.
AC	P05C9; Q9CB56;
ID	Y500A MYCTU STANDARD; PRT; 33 AA.
AC	P05C9; Q9CB56;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Hypothetical protein Rv0500.1/wnt0521.1; ORFName=Rv0500B; GN
OS	Mycobacterium tuberculosis.
OC	Bacteria; Actinobacteria; Actinomycetales;
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC	Mycobacterium tuberculosis complex.
OX	NCBI_TaxID=1773;
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX	STRAIN=H37Rv;
RX	MEDLINE=9825987; PubMed=9634230; DOI=10.1038/31159;
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Telkwa F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Honby T., Jaget K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skeleton S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence,"; Nature 393:537-544 (1998).
RN	[2]
RX	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=CDC 1551 / Oshkosh;
RX	MEDLINE=22205494; PubMed=12218036;
RA	DOL=10.1128/JB.184.19.5479-5490.2002; Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O., Peterson J.D., Deboy R.T., Dodson R.K., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermoljeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weiman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Frazer C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains,"; J. Bacteriol. 184:5479-5490(2002).
RN	[3]
RP	IDENTIFICATION.
RC	STRAIN=H37Rv;
RX	MEDLINE=22255591; PubMed=12336843;
RA	Camer J.-C., Pryor M.J., Medigue C., Cole S.T.; "Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv,"; Microbiology 148:2967-2973(2002).
CC	--
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	--
CC	EMBL; AL53925; CAC1945.1; -; Genomic_DNA.
DR	PIR; A87213; A87213.
DR	Leproma; ML2428R; -.
KW	Complete proteome; Hypothetical protein.
SEQUENCE	33 AA; 4145 MW; 8156A587FL291FS CRC64;
SQ	SEQUENCE 33 AA; 4145 MW; 8156A587FL291FS CRC64;

RESULT 15
 Q9UGR5_CABEL
 ID Q9UGR5_CABEL PRELIMINARY;
 AC Q9UGR5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Cyclin-dependent kinase inhibitor (Hypothetical protein cki-2).
 GN Nameck-2; ORFName=T05A6.2; T05A6.2B;
 OS Cenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis;
 NCBI_TaxID=6339;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=N2; Bristol;
 RX MEDLINE=2005449; PubMed=10597644; DOI=10.1038/70272;
 RA Feng H., Zhong W., Punkosdy G., Gu S., Zhou L., Seabolt E.K.,
 RA Kireos S.T.;
 RT "CUL-2 is required for the G1-to-S-phase transition and mitotic
 chromosome condensation in *Caenorhabditis elegans*.";
 RL Nat. Cell Biol. 1:486-492 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=9906013; PubMed=9851916;
 RG The *C. elegans* sequencing consortium;
 RT "Genome sequencing of the nematode *C. elegans*: a platform for
 investigating biology.,"
 RL Science 282:2012-2018 (1998).
 DR EMBL; AP179359; AAFL3869.1; -; mRNA.
 DR EMBL; Z50796; CADP5597.1; -; Genomic_DNA.
 DR Ensembl; T05A6.2; Caenorhabditis elegans.
 DR WormBase; WBGene0000517; cki-2.
 DR WormRep; T05A6.2b; CE31824.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR03175; CDI.
 DR Pfam; PF02234; CDI.1.
 KW Complete proteome; Cyclin; Hypothetical protein; Kinase.
 SQ SEQUENCE 259 AA; 28651 MW; 904F9814A9897EA8 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 259;
 Best local similarity 66.7%; Pred. No. 51;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RKLMLKSTRROR 12
 DB 241 KKMKTISTRRSR 252

Search completed: February 4, 2006, 03:41:25
 Job time : 139.556 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model
 Run on: February 4, 2006, 03:41:44 ; Search time 30.6667 Seconds
 (without alignments)
 32.351 Million cell updates/sec

Title: US-10-790-768A-1
 perfect score: 58 Sequence: 1 RKLKSTRRQR 12

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
 Searched:

572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Maximum Match 0% Listing first 45 summaries

Database : Issued Patents AA: *
 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
 4: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep: *
 5: /cgn2_6/ptodata/1/1aa/RB_COMB.pep: *
 6: /cgn2_6/ptodata/1/1aa/backfillseq1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	33	2 US-09-605-703B-2766	Sequence 2766, AP
2	39	67.2	131	2 US-09-511-991A-8105	Sequence 8105, AP
3	36	62.1	161	2 US-09-252-991A-27639	Sequence 27639, AP
4	36	62.1	153	2 US-09-252-991A-25958	Sequence 25958, AP
5	60.3	87	2	US-03-248-796A-25921	Sequence 25921, AP
6	35	60.3	157	1 US-08-630-82A-60	Sequence 60, AP
7	35	60.3	157	1 US-03-005-069-60	Sequence 60, AP
8	35	60.3	157	2 US-03-171-156A-18	Sequence 18, AP
9	35	60.3	157	2 US-09-004-730A-18	Sequence 18, AP
10	35	60.3	157	2 US-08-981-799A-18	Sequence 18, AP
11	35	60.3	220	2 US-03-134-00C-3832	Sequence 3832, AP
12	35	60.3	660	2 US-09-252-991A-22842	Sequence 22842, AP
13	35	60.3	725	2 US-09-252-991A-23752	Sequence 23752, AP
14	35	60.3	879	1 US-03-554-612C-1	RESULT 2
15	34	58.6	67	2 US-09-270-767-60600	Sequence 8105, Application US/09513999C
16	34	58.6	105	2 US-09-270-767-59291	Patent No. 678361
17	34	58.6	125	2 US-09-270-767-45108	GENERAL INFORMATION:
18	34	59.6	154	2 US-09-252-991A-20018	APPLICANT: Dumas Milne Edwards, J.B.
19	34	58.6	271	2 US-09-252-991A-23448	APPLICANT: Duclert, A.
20	34	58.6	285	2 US-03-252-991A-18133	APPLICANT: Giordano, J.Y.
21	34	58.6	321	2 US-09-489-039A-10010	APPLICANT: Giordano, J.Y.
22	34	58.6	367	2 US-09-270-767-33888	TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Protein.
23	34	58.6	514	2 US-09-800-722-124	Patent No. 678361
24	34	58.6	575	2 US-10-104-047-2221	FILE REFERENCE: 59.US2.REG
25	34	58.6	1038	2 US-09-081-385-151	CURRENT APPLICATION NUMBER: US/09/513,999C
26	34	58.6	1038	2 US-09-752-639-151	CURRENT FILING DATE: 2000-02-24
27	2	US-09-712-813-151	1038	2 US-09-712-813-151	PRIOR APPLICATION NUMBER: US 60/122,487

ALIGNMENTS

RESULT 1
 US-09-605-703B-2766
 Sequence 2766, Application US/09605703B
 ; Patent No. 6962989

; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS
 ; FILE REFERENCE: BGI-129P
 ; CURRENT APPLICATION NUMBER: US/09/605,703B
 ; CURRENT FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/142,764
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/152,318
 ; NUMBER OF SEQ ID NOS: 2934
 ; SEQ ID NO 2766
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-605-703B-2766

Query Match 72.4%; Score 42; DB 2; Length 33;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY ||||:|||||
 1 RKLKSTRRQR 12
 Db 18 RKLKSTRRQR 29

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; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 8105
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 24
; OTHER INFORMATION: Xaa=Cys or Tyr
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 107
; OTHER INFORMATION: Xaa= * or Cys or Trp
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 120
; OTHER INFORMATION: Xaa= * or Ieu or Ser or Trp
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 121
; OTHER INFORMATION: Xaa=Met or Val
; FEATURE: NAME/KEY: UNSURE
; LOCATION: 131
; OTHER INFORMATION: Xaa=Ala or Thr
; US-09-513-999C-8105

Query Match 67.2%; Score 39; DB 2; Length 131;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRORR 12
Db 51 KQLLKSRRRK 62

RESULT 3
US-09-232-991A-27639
; Sequence 27639, Application US/09252991A
; Patent No. 655195
; GENERAL INFORMATION:
; APPLICANT: MARC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27639
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-27639

Query Match 62.1%; Score 36; DB 2; Length 161;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRORR 12
Db 2 RKKWKSRRRK 13

RESULT 4
US-09-252-991A-27639
; Sequence 27639, Application US/09252991A
; Patent No. 655195
; GENERAL INFORMATION:
; APPLICANT: FRANK, GLENN R.
; APPLICANT: HUNTER, SHIRLEY WU
; APPLICANT: WALLENFELS, LYNDIA
; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado

RESULT 5
US-09-448-796A-25921
; Sequence 25921, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Wainstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107195.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074, 725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096, 409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 24208
; SEQ ID NO 25921
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-25921

Query Match 60.3%; Score 35; DB 2; Length 87;
Best Local Similarity 58.3%; Pred. No. 71;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RKLMLKSTRRORR 12
Db 12 RKLMLKKNLKR 23

RESULT 6
US-08-620-822A-60
; Sequence 60, Application US/08630822A
; Patent No. 5840595
; GENERAL INFORMATION:
; APPLICANT: FRANK, GLENN R.
; APPLICANT: HUNTER, SHIRLEY WU
; APPLICANT: WALLENFELS, LYNDIA
; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado

```

COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/630,822A
 FILING DATE: 11-APR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CONNELL, GARY J.
 REFERENCE NUMBER: 32,020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 157 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-630-822A-60

RESULT 7

Query Match Best Local Similarity 70.0%; Score 35; DB 1; Length 157;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1 RKLMLKSTRQQ	10
Db	100 RKVLESVRQQ	109

US-09-005-069-60

RESULT 8

Query Match Best Local Similarity 70.0%; Score 35; DB 1; Length 157;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1 RKLMLKSTRQQ	10
----	---------------	----

US-09-171-156A-18

Sequence 18, Application US/09171156A
 PATENT NO. 6368846
 GENERAL INFORMATION:
 APPLICANT: Hunter, Shirley Wu
 ADDRESS: 1560 BROADWAY, SUITE 1200
 CITY: DENVER
 STATE: CO
 COUNTRY: U.S.A.
 ZIP: 80202

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS

NUMBER OF SEQUENCES: 83
 CORRESPONDENCE ADDRESS:
 ADDRESSER: SHERIDAN ROSS P.C.
 STREET: 1560 BROADWAY, SUITE 1200
 CITY: DENVER
 STATE: CO
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/171,156A
 FILING DATE: 04-Mar-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REFERENCE NUMBER: 32,020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/863-9700
 TELFAX: 303/863-0223
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 157 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-171-156A-18

RESULT 9

Query Match Best Local Similarity 70.0%; Score 35; DB 2; Length 157;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1 RKLMLKSTRQQ	10
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US-09-004-730A-18

Sequence 18, Application US/09004730A
 PATENT NO. 648968
 GENERAL INFORMATION:

APPLICANT: Weber, Eric
 APPLICANT: Wu Hunter, Shirley
 APPLICANT: Sim, Gek-Kee
 APPLICANT: Frank, Glenn
 APPLICANT: Wallenfelz, Lynda
 TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH
 FILE REFERENCE: 2618-17-C5-PUS-1
 CURRENT APPLICATION NUMBER: US/09/004,730A
 PRIORITY FILING DATE: 1998-01-08
 PRIOR APPLICATION NUMBER: PCT/97US/18669
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 150
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 18
 LENGTH: 157
 TYPE: PRT
 ORGANISM: Ctenocephalides felis
 US-09-004-730A-18

Query Match 60.3%; Score 35; DB 2; Length 157;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQ 10
 Db 100 RKVLESVRQQ 109

RESULT 10
 US-08-981-799A-18

Sequence 18 Application US/08981799A
 Patent No. 657638
 GENERAL INFORMATION:
 APPLICANT: Weber, Eric
 APPLICANT: Wu Hunter, Shirley
 APPLICANT: Sim, Gek-Kee
 APPLICANT: Frank, Glenn
 APPLICANT: Wallenfelz, Lynda
 TITLE OF INVENTION: "NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH"
 FILE REFERENCE: 2618-17-C5-PUS
 CURRENT APPLICATION NUMBER: US/08/981,799A
 CURRENT FILING DATE: 1998-08-27
 PRIORITY FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 150
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 18
 LENGTH: 157
 TYPE: PRT
 ORGANISM: Ctenocephalides felis
 US-08-981-799A-18

Query Match 60.3%; Score 35; DB 2; Length 157;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQ 10
 Db 100 RKVLESVRQQ 109

RESULT 11
 US-09-114-000C-3832

Query Match 60.3%; Score 35; DB 2; Length 157;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQ 10
 Db 100 RKVLESVRQQ 109

RESULT 12
 US-09-252-991A-22842

Query Match 60.3%; Score 35; DB 2; Length 220;
 Best Local Similarity 87.5%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSTRRQR 12
 Db 1 KSTRRKR 8

RESULT 13
 US-09-252-991A-22842

Query Match 60.3%; Score 35; DB 2; Length 660;
 Best Local Similarity 58.3%; Pred. No. 4.4e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQ 12
 Db 603 RROLPOQRQR 614

RESULT 13
 US-09-232-991A-23752

Query Match 60.3%; Score 35; DB 2; Length 725;
 Best Local Similarity 58.3%; Pred. No. 4.4e+02; Indels 0; Gaps 0;

QY 1 RKLMLKSTRRQ 10
 Db 603 RROLPOQRQR 614

Query Match 60.3%; Score 35; DB 2; Length 725;

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-03-18
 PRIORITY FILING DATE: 1998-02-18
 PRIORITY APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 23752
 LENGTH: 725
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23752

Query Match 60.3%; Score 35; DB 2; Length 725;

Best Local Similarity 58.3%; Pred. No. 4.8e+02; Mismatches 4; Indels 0; Gaps 0;
 Matches 7; Conservative 1; US-08-554-612C-1

Qy 1 RKMKSTRQR 12
 Db 647 RQDPRQRQR 658

RESULT 14
 US-08-554-612C-1
 Sequence 1, Application US/08554612C
 Patent No. 5747660
 GENERAL INFORMATION:
 APPLICANT: Orlicky, David
 TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
 TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC-compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/554.612C
 FILING DATE: NO. 5747660ember 6, 1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela
 REGISTRATION NUMBER: 36 677
 REFERENCE/DOCKET NUMBER: 06519/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 322-5070
 TELEFAX: (415) 854-0875
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 879 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-554-612C-1

Query Match 58.6%; Score 34; DB 2; Length 67;
 Best Local Similarity 87.5%; Pred. No. 81; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 1; US-09-270-767-60600

Qy 1 RKMKSTRQR 8
 Db 13 RKVLRKR 20

Search completed: February 4, 2006, 03:43:33
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RESULT 15
 US-09-270-767-60600
 Sequence 60600, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 FILE REFERENCE: File Reference: 7356-094
 CURRENT APPLICATION NUMBER: US/09270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 60600
 LENGTH: 67
 TYPE: PRT
 ORGANISM: *Drosophila melanogaster*

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OM protein - protein search, using SW model

Run on: February 4, 2006, 03:42:34 ; Search time 104 Seconds
 (without alignments)
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Title: US-10-790-768A-1
 Perfect score: 58
 Sequence: 1 RKLKSTRRQR 12

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 Gapop 10.0 , Gapext 0.5

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 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:

1867569

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications AA_Main.*

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SUMMARIES

* Query

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4	58	100.0	15	US-10-790-768A-16
5	58	100.0	21	US-10-790-768A-4
6	58	100.0	21	US-10-790-768A-19
7	58	100.0	21	US-10-790-768A-20
8	58	100.0	27	US-10-790-768A-5
9	48	82.8	19	US-10-790-768A-18
10	48	82.8	25	US-10-790-768A-21
11	48	82.8	25	US-10-790-768A-22
12	43	74.1	247	US-10-408-765A-2219
13	42	72.4	33	US-09-73B-626-3964
14	40	69.0	121	US-10-431-963-113033
15	40	69.0	691	US-10-156-761-8521
16	39	67.2	33	US-10-080-170-579
17	39	67.2	33	US-10-080-170-405
18	39	67.2	33	US-10-080-170-279
19	39	67.2	33	US-10-080-170-405
20	39	67.2	33	US-10-468-356-279
21	39	67.2	33	US-10-468-356-405
22	39	67.2	129	US-10-767-701-62017
23	39	67.2	258	US-10-369-493-5460
24	38	65.5	50	US-10-741-600-1197
25	37	63.8	177	US-10-767-701-56381
26	37	63.8	193	US-10-767-701-58463
27	37	63.8	4	US-10-437-963-147451

ALIGNMENTS

RESULT 1
 US-10-790-768A-1
 ; Sequence 1, Application US/10790768A
 ; Publication No. US20040209797A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karas, Michael
 ; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
 ; FILE REFERENCE: 002877.00028
 ; CURRENT APPLICATION NUMBER: US/10/790-768A
 ; CURRENT FILING DATE: 2004-03-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: protein transduction domain

US-10-790-768A-1
 ; Query Match 100.0%; Score 58; DB 4; Length 12;
 ; Best Local Similarity 100.0%; Pred. No. 0.0027%; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 12; Conservative 0;
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Query Match 100.0%; Score 58; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0034; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKLKSTRRQR 12
 Db 4 RKLKSTRRQR 15

RESULT 3 US-10-790-768a-14
 Sequence 14, Application US/10790768A
 Publication No. US20040209797A1
 GENERAL INFORMATION:
 APPLICANT: Karas, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acid Reference: 002877.00028
 CURRENT APPLICATION NUMBER: US/10/790,768A
 CURRENT FILING DATE: 2004-03-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 14
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: protein transduction domain
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(1)
 OTHER INFORMATION: Biotin
 US-10-790-768a-14

Query Match 100.0%; Score 58; DB 4; length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0034; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKLKSTRRQR 12
 Db 4 RKLKSTRRQR 15

RESULT 4 US-10-790-768a-16
 Sequence 16, Application US/10790768A
 Publication No. US20040209797A1
 GENERAL INFORMATION:
 APPLICANT: Karas, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acid Reference: 002877.00028
 CURRENT APPLICATION NUMBER: US/10/790,768A
 CURRENT FILING DATE: 2004-03-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: protein transduction domain
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(1)
 OTHER INFORMATION: Biotin
 US-10-790-768a-16

Query Match 100.0%; Score 58; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0034; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKLKSTRRQR 12
 Db 4 RKLKSTRRQR 15

RESULT 5 US-10-790-768a-4
 Sequence 4, Application US/10790768A
 Publication No. US20040209797A1
 GENERAL INFORMATION:
 APPLICANT: Karas, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acid Reference: 002877.00028
 CURRENT APPLICATION NUMBER: US/10/790,768A
 CURRENT FILING DATE: 2004-03-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: protein transduction domain
 US-10-790-768a-4

Query Match 100.0%; Score 58; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0048; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKLKSTRRQR 12
 Db 4 RKLKSTRRQR 15

RESULT 6 US-10-790-768a-19
 Sequence 19, Application US/10790768A
 Publication No. US20040209797A1
 GENERAL INFORMATION:
 APPLICANT: Karas, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acid Reference: 002877.00028
 CURRENT APPLICATION NUMBER: US/10/790,768A
 CURRENT FILING DATE: 2004-03-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 19
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: protein transduction domain
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(1)
 OTHER INFORMATION: Biotin
 US-10-790-768a-19

Query Match 100.0%; Score 58; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0048; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKLKSTRRQR 12
 Db 4 RKLKSTRRQR 15

RESULT 7 US-10-790-768a-20
 Sequence 20, Application US/10790768A
 Publication No. US20040209797A1

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; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/10/790, 768A
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: protein transduction domain
; NAME/KEY: MISC_FEATURE
; LOCATION: (1).(1)
; OTHER INFORMATION: Biotin
; OTHER INFORMATION: Biotin
; US-10-790-768A-20

Query Match          100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 RKLKSTRRQR 12
Db      10 RKLKSTRRQR 21

RESULT 8
US-10-790-768A-5
; Sequence 5, Application US/10/790768A
; Publication No. US20040209797A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/10/790, 768A
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; FEATURE: OTHER INFORMATION: protein transduction domain
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: protein transduction domain
; US-10-790-768A-5

Query Match          100.0%; Score 58; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0062; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 RKLKSTRRQR 12
Db      10 RKLKSTRRQR 21

RESULT 9
US-10-790-768A-18
; Sequence 18, Application US/10/790768A
; Publication No. US20040209797A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/10/790, 768A
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: protein transduction domain
; NAME/KEY: MISC_FEATURE
; LOCATION: (1).(1)
; OTHER INFORMATION: Biotin
; OTHER INFORMATION: Biotin
; US-10-790-768A-18

Query Match          82.8%; Score 48; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      3 MLKSTRRQR 12
Db      10 MLKSTRRQR 19

RESULT 10
US-10-790-768A-21
; Sequence 21, Application US/10/790768A
; Publication No. US20040209797A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/10/790, 768A
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: protein transduction domain
; NAME/KEY: MISC_FEATURE
; LOCATION: (1).(1)
; OTHER INFORMATION: Biotin
; OTHER INFORMATION: Biotin
; US-10-790-768A-21

Query Match          82.8%; Score 48; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      3 MLKSTRRQR 12
Db      10 MLKSTRRQR 19

RESULT 11
US-10-790-768A-22
; Sequence 22, Application US/10/790768A
; Publication No. US20040209797A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/10/790, 768A
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: protein transduction domain
; NAME/KEY: MISC_FEATURE
; LOCATION: (1).(1)
; OTHER INFORMATION: Biotin
; OTHER INFORMATION: Biotin
; US-10-790-768A-22

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OTHER INFORMATION: protein transduction domain
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(1)
 OTHER INFORMATION: Biotin
 US-10-790-768a-22

Qy	3 MLKSTRRQR 12	Qy	16 MLKSTRRQR 25	Db
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RESULT 12

US-10-408-765A-2219

Sequence 2219, Application US/10408765A
 Publication No. US20040101874A1
 GENERAL INFORMATION:
 APPLICANT: Ghosh, Sunmitra S.
 APPLICANT: Fany, Eoin D.
 APPLICANT: Zhang, Bing
 APPLICANT: Gibson, Bradford W.
 APPLICANT: Taylor, Steven W.
 APPLICANT: Glenn, Gary M.
 APPLICANT: Warnock, Dale E.
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 FILE REFERENCE: 660088.455
 CURRENT APPLICATION NUMBER: US/10/408,765A
 CURRENT FILING DATE: 2003-04-04
 NUMBER OF SEQ ID NOS: 3077
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2219
 LENGTH: 247
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-408-765A-2219

RESULT 13

US-09-730-623964

Sequence 3964, Application US/09738626
 Publication No. US2003019705A1
 GENERAL INFORMATION:
 APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOGUCHI, HIROSHI
 APPLICANT: ANDO, SEIJI
 APPLICANT: HAYASHI, MIKIRO
 APPLICANT: OCHIAI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOH, AKIHIRO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US/09/738,626
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: JP 99/377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07

Query Match Best Local Similarity 82.8%; Score 48; DB 4; Length 25;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RKLMLKSTRRQR 11	Qy	1 RKLMLKSTRRQR 140	Db
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RESULT 14

US-10-437-963-113033

Sequence 113033, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalec, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukhakov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Jing
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5322)1B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 113033
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_16860C.1.pep
 US-10-437-963-113033

Query Match Best Local Similarity 74.1%; Score 43; DB 4; Length 247;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1 RKLMLKSTRRQR 11	Qy	1 RKLMLKSTRRQR 12	Db
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RESULT 15

US-10-156-761-8521

Sequence 8521, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HONIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHITAKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8521
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8521

Query Match 69.0%; Score 40; DB 4; Length 691;
Best Local Similarity 66.7%; Fred. No. 1.9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservatve 2;
QY 1 RKMUKSTRROR 12
| : | |||||
Db 359 RRLRLASRRROR 370

Search completed: February 4, 2006, 03:47:33
Job time : 105 sec^s

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GenCore version 5.1.7																		
Copyright (C) 1993 - 2006 Biocceleration Ltd.																		
OM protein - protein search, using bw model																		
Run on: February 4, 2006, 03:26:33 ; Search time 310.556 seconds																		
(without alignment) 21.1222 Million cell updates/sec																		
Title:	Total number of hits satisfying chosen parameters: 2443163																	
Perfect score:	Minimum DB seq length: 0																	
Sequence:	Maximum DB seq length: 200000000																	
Post-processing: Minimum Match 0% Maximum Match 100%																		
Listing first 45 summaries																		
Database :	A_Geneseq 21;*																	
1:	geneseqp1980s;*																	
2:	geneseqp1990s;*																	
3:	geneseqp2000s;*																	
4:	geneseqp2001s;*																	
5:	geneseqp2002s;*																	
6:	geneseqp2003as;*																	
7:	geneseqp2004as;*																	
8:	geneseqp2005s;*																	
9:	geneseqp2005s;*																	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																		
SUMMARIES																		
Result No.	Score	Query	Match Length	DB ID	Description	Key	Modified-site	Location/Qualifiers	ALIGNMENTS									
1	75	100.0	15	BDS17630	RESULT 1 ADS17630	PN	W02004078933-A2.	I /note= "biotin attached"										
2	75	100.0	15	ADS17618	ID ADS17630 standard; peptide; 15 AA.	XX												
3	75	100.0	21	ADS17636	AC ADS17630;	XX												
4	75	100.0	21	ADS17620	DT 02-DEC-2004 (first entry)	XX												
5	75	100.0	21	ADS17635	DE Amino acid sequence of a PTD designated Biotin-Lys-InvRPS.	XX												
6	70	93.3	15	ADS17632	KW protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide; cell transport.	XX												
7	62	82.7	27	ADS17621	KW Synthetic.	XX												
8	60	80.0	19	ADS17634	XX													
9	60	80.0	25	ADS17638	PH													
10	60	80.0	25	ADS17637	FT													
11	58	77.3	12	ADS17617	FT 03-MAR-2004; 2003US-0451243P.	PR												
12	44	58.7	63	ADS17617	FT 03-MAR-2004; 2004US-00790768.	PR												
13	44	58.7	63	ADS17617	XX													
14	57.3	33	6	ABM47044	(BIOW-) BIOWHITTAKER TECHNOLOGIES INC.	PA												
15	57.3	247	7	ABD170413	XX													
16	42	174	7	ADCS94072	PI Karab M;	PT												
17	42	56.0	4	ADP04119	XX													
18	42	56.0	537	ABD077212	DR MPI; 2004-653708/63.	XX												
19	42	56.0	617	ABM88910	XX													
20	42	56.0	708	ABG90210	PT New isolated and purified polypeptide with a protein transduction domain, used for delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell.	PT												
21	41	54.7	413	AYV41728	XX													
22	41	54.7	413	ABG4284	CC amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in pro-cargo moiety complexes that can reversibly immortalise	CC												
23	41	54.7	413	ABU29101	CC cells and increase cell viability in culture. The present sequence	CC												
24	54.7	413	5	ABU82731	CC													

CC represents PTD peptide used in an experiment to determine the transduction efficiency of inverted isomers of PTD_B.

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 75; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGGRKMLKSTRRQR 15
Db 1 KGGRKMLKSTRRQR 15

RESULT 2
ADS17618
ID ADS17618 Standard; peptide; 15 AA.

XX AC ADS17636;
XX DT 02-DEC-2004 (first entry)

DE Amino acid sequence of a PTD designated peptide 15.
XX protein transduction domain; PTD; PTD-cargo moiety complex;
KW protein transduction domain; PTD; PTD-cargo moiety complex;
KW cell immortalisation; cell viability; internalising peptide;
KW cell transport.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "biotin attached"

XX PN WO2004078933-A2.
XX PD 16-SEP-2004.
XX PR 04-MAR-2004; 2004WO-US006445.
XX PT 04-MAR-2003; 2003US-0451243P.
XX PR 03-MAR-2004; 2004US-00790768.

XX PA (BIOW-) BIOWHITTAKER TECHNOLOGIES INC.

XX PI Karab M;
XX DR WPI; 2004-653708/63.
XX PS New isolated and purified polypeptide with a protein transduction domain, useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.

XX Example 10; SEQ ID NO 20; 60pp; English.

The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 75; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGGRKMLKSTRRQR 15
Db 1 KGGRKMLKSTRRQR 15

RESULT 4
ADS17620
ID ADS17620 Standard; peptide; 21 AA.

XX AC ADS17620;
XX DT 02-DEC-2004 (first entry)

DE Amino acid sequence of protein transduction domain (PTD) peptide #3.
XX protein transduction domain; PTD; PTD-cargo moiety complex;
KW protein transduction domain; PTD; PTD-cargo moiety complex;
KW cell immortalisation; cell viability; internalising peptide;
KW cell transport.

XX

RESULT 3
ADS17636
ID ADS17636 Standard; peptide; 21 AA.

CC transduction domain (PTD), and are capable of delivering small molecules, CC proteins, and nucleic acids to an intracellular compartment of a cell. An CC amino terminal lysine linker improves the efficiency of the PTD. The PTD CC can be used in PTD-cargo moiety complexes that can reversibly immortalise CC cells and increase cell viability in culture. The present sequence represents PTD peptide used in an experiment to determine the transduction efficiency of inverted isomers of PTDs.

SQ Sequence 15 AA;

Query Match 93.3%; Score 70; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGRMLKSTRRQR 15
Db 2 GGRMLKSTRRQR 15

RESULT 8
ADS17634 standard; peptide, 19 AA.
ID ADS17634
XX
AC ADS17634;
XX DT 02-DEC-2004 (first entry)
XX DE Amino acid sequence of a PTD designated Peptide 13.
XX KW protein transduction domain; PTD; PTD-cargo moiety complex;
KW cell immortalisation; cell viability; internalising peptide;
KW cell transport.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "biotin attached"
XX PN WO2004078933-A2.
PN 16-SEP-2004.
XX PD 04-MAR-2004; 2004WO-US006445.
XX PR 04-MAR-2003; 2003US-0451243P.
PR 03-MAR-2004; 2004US-00790788.
XX PA (BLOW-) BIOMHITTAKER TECHNOLOGIES INC.
XX PI Karas M;
XX DR WPI; 2004-653708/63.
XX PT New isolated and purified polypeptide with a protein transduction domain,
PT useful for delivering small molecules, proteins and nucleic acids to an
PT intracellular compartment of a cell.
XX PS Example 10; SEQ ID NO 18; 60pp; English.

The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety complex.

SQ Sequence 19 AA;

Query Match 80.0%; Score 60; DB 8; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.0098; Mismatches 0; Indels 4; Gaps 1;

Matches 14; Conservative 1; Mismatches 0; Indels 6; Gaps 1;
Qy 1 KGGK---MLKSTRRQR 15
Db 1 KGGKKRKVNLKSTRRQR 19

RESULT 9

ADS17638 standard; peptide, 25 AA.

Query Match 82.7%; Score 62; DB 8; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.0065; Mismatches 0; Indels 6; Gaps 1;

Matches 15; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
Qy 1 KGGKKRKVNLKSTRRQR 15
Db 1 KGGKKRKVNLKSTRRQR 21

CC via this method; a vaccine composition (comprising *P. acnes* polypeptides, CC polynucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit CC for detecting or determining the presence or absence of *P. acnes* in a patient; and a method for inhibiting the development of *P. acnes* in a patient; and a method for inhibiting the development of *P. acnes* in a patient; and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the *P. acnes* polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 63 AA;

Query Match 58.7%; Score 44; DB 6; Length 63;

Best Local Similarity 66.7%; Pred. No. 13; Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KGGRKMLKSTRRQRR 15

Db 45 KKHKKLKLKKTRRIQR 59

RESULT 14

AAG90210 ID AAG90210 standard; protein; 33 AA.

XX AC AAG90210;

XX DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 3964.

XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.

XX OS Corynebacterium glutamicum.

XX PN EP1108790-A2.

XX PD 20-JUN-2001.

XX PR 18-DEC-2000; 2000EP-0012768B.

XX PR 16-DEC-1999; 990P-00377484.

PR 07-APR-2000; 2000EP-00159162.

PR 01-AUG-2000; 2000EP-0028098B.

XX PA (KYOU) KYOWA HAKKO KOGYO KK.

XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR WPI; 2001-376931/40.

DR N-PSDB; AAH65429.

XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.

XX PT Claim 17; SEQ ID NO 3964; 246pp + Sequence Listing; English.

XX CC The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium *Corynebacterium glutamicum*. These sequences are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing

CC the expression profile or expression pattern of a gene derived from CC *Coryneform bacterium*, and identifying a homologue of a gene derived from CC *Coryneform bacterium*. *Coryneform bacteria* are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-leucine. The present sequence is a protein described in the specification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

SQ Sequence 33 AA;

Query Match 57.3%; Score 43; DB 4; Length 33;

Best Local Similarity 66.7%; Pred. No. 10; Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KGGRKMLKSTRRQRR 15

Db 15 KKHKKLKLKKTRRIQR 29

RESULT 15

ADD70413 ID ADD70413 standard; protein; 247 AA.

XX AC ADD70413;

XX DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2219.

XX KW mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PR 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DB;

XX DR WPI; 2003-8453369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprising detecting a modified polypeptide in a sample and correlating PT with the disease.

XX PS Claim 1; SEQ ID NO 2219; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytosolic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX

SQ Sequence 247 AA;

Query Match 57.3%; Score 43; DB 7; Length 247;
Best local similarity 81.8%; Pred. No. 71;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 RKLMLKSTRROR 14
Db 130 RKSLSLKSTRRR 140

Search completed: February 4, 2006, 03:36:14
Job time : 313.056 secs

OM protein - protein search, using sw model	GenCore version 5.1.7		
Run on:	Copyright (c) 1993 - 2006 Biocceleration Ltd.		
	February 4, 2006, 03:36:41 ; Search time 28.3333 Seconds		
	(without alignments)		
Title:	US-10-790-768A-2		
Perfect score:	75		
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scoring table:	BLOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	283416 seqs, 96216763 residues		
Total number of hits satisfying chosen parameters:	283416		
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing:	Minimum Match 0%		
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	Listing first 45 summaries		
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1:	pir1:*		
2:	pir2:*		
3:	pir3:*		
4:	pir4:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
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1	44	58.7 77 2 B40973	spERMATID-SPECIFIC protein T2 precursor - common cuttlefish Nt_Alternate_name: arginine-rich Protamine; testis-specific protein T2 C_Species: Sepia officinalis (common cuttlefish)
2	44	58.7 78 2 A40973	C_SpecieS: Sepia officinalis (common cuttlefish)
3	44	58.7 79 2 S56116	C_Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
4	43	57.3 32 2 T32675	C_Accession: B40973; S14086
5	42	56.0 69 2 S39424	R_Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Pontieu, A.; Boutillon, C.; Van Dorst, J. Biol. Chem. 266, 17388-17395, 1991
6	41	54.7 1017 2 T31354	A_Title: Cuttlefish SPERMATID-SPECIFIC protein T. Molecular characterization of two variants
7	40	53.3 33 2 A87213	A_Reference_number: A40973; MUID:91373359; PMID:1894625
8	40	53.3 357 2 S43220	A_Accesion: B40973
9	40	53.3 361 2 A87979	A_Molecule_type: Protein
10	40	53.3 441 2 D95124	A_Residues: 1-77 <WOU>
11	40	53.3 441 2 F97994	A_Cross-references: UNIPROT:P80002; UNIPARC:UPI00001323AB
12	39	52.0 44 2 AGI430	R_Martin-Pontieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van Dorst, J. Biol. Chem. 265, 611-619, 1990
13	39	52.0 44 2 ARB805	A_RefereCe number: S14085; MUID:91153298; PMID:1999185
14	39	52.0 118 2 S56117	A_Accession: S14086
15	39	52.0 258 2 T24499	A_Molecule_type: protein
16	39	52.0 419 2 S61803	A_Residues: 22-77 <MAP>
17	39	52.0 836 2 T21631	A_Cross-references: UNIPARC:UPI00001771F9
18	38	50.7 261 1 AGI596	C_Superfamily: sperm histone
19	38	50.7 305 1 NKVNLHH	C_Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis
20	38	50.7 408 2 EB8743	F1-21-Domain: signal sequence status predicted <SG>
21	38	50.7 426 2 B96519	F22-77-/Product: protamine variant Sp2 #status experimental <MAP>
22	38	50.7 489 2 S55428	Query Match 58.7%; Score 44; DB 2; Length 77;
23	38	50.7 507 2 AC036	Best Local Similarity 53.3%; Pred. No. 2,3; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
24	38	50.7 507 2 H98249	Qry 1 KGGRIKQLKSTRRQRR 15
25	38	50.7 556 2 C9037	DB 19 KGGRRRRRSRRRR 33
26	38	50.7 934 2 H90195	RESULT 2
27	38	50.7 1020 2 EB8165	A0973
28	37	49.3 44 2 C493396	SPERMATID-SPECIFIC protein T1 precursor - common cuttlefish
29	49.3 45 2 B58208	Nt_Alternate_name: arginine-rich protamine; testis-specific protein T1	
		C_Species: Sepia officinalis (common cuttlefish)	
		C_Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004	
		C_Accession: A40973; S14085	
		R_Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Pontieu, A.; Boutillon, C.; Van Dorst, J. Biol. Chem. 266, 17388-17395, 1991	
		A_Title: Cuttlefish SPERMATID-SPECIFIC protein T. Molecular characterization of two variants	
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		A_Molecule_type: protein	
		A_Residues: 1-78 <WOU>	
		A_Cross-references: UNIPROT:P80001; UNIPARC:UPI00001323A4	
ALIGNMENTS			

R; Martin-Pontieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; var
 Eur. J. Biochem. 195, 611-19, 1991
 A; Title: Cuttlefish sperm protamines. I. Amino acid sequences of two distinct variants.
 A; Reference number: S14085; MUID:91153298; PMID:1999185
 A; Accession: S14085
 A; Residues: 22-78 <MAR>
 A; Cross-references: UNIPARC:UPI00001771PB
 C; Superfamily: sperm histone
 C; Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis
 F; 1-21/Domain: signal sequence #status predicted <SG>
 F; 22-78/Product: protamine variant SpI #status experimental <MAT>
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 Best Local Similarity 53.3%; Pred. No. 2.3;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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 Db 19 KGGRRRRRRSRRR 33

RESULT 3
 S6616
 A; Residues: Squid spermocogenesis; molecular characterization of testis-specific pro-protami
 A; Reference number: S56116; MUID:95351983; PMID:7626016
 A; Accession: S56116
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-79 <WQO>
 C; Superfamily: sperm histone
 C; Keywords: sperm histone

Query Match 58.7%; Score 44; DB 2; Length 79;
 Best Local Similarity 53.3%; Pred. No. 2.3;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 19 KGGRRRRRRSRRR 33

RESULT 4
 T36225
 C; Species: Streptomyces coelicolor
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C; Accession: T36225
 R; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A; Reference number: Z21576
 A; Accession: T36225
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Residues: 1-32 <WQR>
 A; Cross-references: UNIPROT:Q9WX07; UNIPARC:UPI00000DB13D; EMBL:ALL079345; PIDN:CAB45361.
 C; Genes:
 A; Gene: SCOE2B-SCE68_25C

Query Match 57.3%; Score 43; DB 2; Length 32;
 Best Local Similarity 66.7%; Pred. No. 1.5;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 15 KGHKRLKLRTRVQRR 29

RESULT 5
 S39424
 C; Species: Tachyglossus aculeatus (Australian echidna)
 C; Protamine PI - Australian echidna
 C; Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C; Accession: S39424
 R; Retief, J.D.; Winkfein, R.J.; Dixon, G.H.
 Eur. J. Biochem. 218, 457-461, 1993
 A; Title: Evolution of the monotremes. The sequences of the protamine PI genes of platypus
 A; Reference number: S39424; MUID:91094837; PMID:8269934
 A; Accession: S39424
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-69 <RET>
 A; Cross-references: UNIPROT:P35311; UNIPARC:UPI000016C71A; EMBL:Z26848; NID:9407183; PIDN:
 C; Genetics:
 A; Introns: 53/1
 C; Superfamily: sperm histone
 C; Keywords: DNA binding

Query Match 56.0%; Score 42; DB 2; Length 69;
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 Qy 3 GRKMLKSTRQR 15
 Db 53 GRRSMRSSLRRR 65

RESULT 6
 T31354
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C; Accession: T31354
 R; Engelund, B.; Neu, A.; Ludwig, J.; Roepke, J.; Pongs, O.
 submitted to the EMBL Data Library, July 1998
 A; Description: Identification of three rat potassium channel genes homologous to D. mela
 A; Reference number: Z22983
 A; Accession: T31354
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-1017 <ENG>
 A; Cross-references: UNIPROT:Q9R1T9; UNIPARC:UPI0000170A85; EMBL:AJ007628; NID:e1329997;
 A; Experimental source: cortex
 C; Genetics:
 A; Gene: elkl1
 C; Keywords: potassium channel

Query Match 54.7%; Score 41; DB 2; Length 1017;
 Best Local Similarity 53.3%; Pred. No. 74;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 160 RGASSRLRSTRQR 174

RESULT 7
 A87213
 C; Species: Mycobacterium leprae
 C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C; Accession: A87213
 C; Accession: A87213
 R; Cole, S.T.; Eigeneier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 Nature 409, 1007-1011, 2001
 A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A; Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A87213
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <STO>
 A;Cross-references: UNIPROT:Q9CB56; UNIPARC:UPI0000139A1B; GB:AL450380; NID:913094003; E
 A;Genetic:
 A;Gene: ML228A

RESULT 8
 S43220
 Query Match 53.3%; Score 40; DB 2; Length 33;
 Best Local Similarity 60.0%; Pred No. 4.9; Mismatches 0;
 Matches 9; Conservative 2; Gaps 0;
 Qy 1 KGAQMKEKTRQR 15
 Db 15 KGRKLRLRTRVQR 29

RESULT 9
 S43220
 Hypothetical protein YER127w - yeast (*Saccharomyces cerevisiae*)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
 C;Accession: S43220; SS0630
 R;Mulligan, J.T.; Dierich, F.S.; Henneberry, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor,
 submitted to the EMBL Data Library, February 1993.
 A;Reference number: S30812
 A;Accession: S43220
 A;Molecule type: DNA
 A;Residues: 1-357 <STO>
 R;Dierich, F.S.
 Submitted to the EMBL Data Library, December 1994
 A;Description: The sequence of *S. cerevisiae* cosmids 9781, 8198, 9115, 9981, and lambda
 A;Reference number: SS0630
 A;Accession: S50630
 A;Molecule type: DNA
 A;Residues: 1-357 <STO>
 C;Cross-references: UNIPARC:UPI0000531FB; EMBL:U18916; NID:g1384128; PIDN: AAC03225.1; E
 A;Gene: SGD:LCP5
 A;Cross-references: SGD:S0000929
 A;Map position: 5R

Query Match 53.3%; **Score** 40; **DB** 2; **Length** 357;
Best Local Similarity 46.7%; **Pred.** No. 4.2; **Mismatches** 0;
Matches 7; **Conservative** 4; **Gaps** 0;
Indels 0;
Qy 1 KGRKMLKSTRRRR 15
Db 271 RGGIKSLRDTKEKRR 285

RESULT 9
 AB1979
 ABC transporter ATP-binding protein alr1364 [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. Strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
 C;Accession: AB1979
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi,
 Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. B, 205:213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MNUID:21595285; PMID:11759840
 A;Accession: AB1979
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-361 <KUR>
 A;Cross-references: UNIPROT:Q8YX34; UNIPARC:UPI00000CE09F; GB:BA000019; PIDN:BAB73341.1;
 A;Experimental source: strain PCC 7120
 A;Genetic:
 A;Gene: alr1364

Query Match 53 3%; Score 40; DB 2; Length 361;
 Best Local Similarity 69 2%; Pred. No. 43;
 Matches 9; Conservative 1; Mismatches 3;
 C;Genetic: Db 120 GLRRRQKSKDRQR 132
 RESULT 10
 D95124
 Glycosyl transferase, group 1 SP1076 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: D95124
 R;Tetteman, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidi
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, T.B.
 Science 293, 498-506, 2001
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MNUID:21357209; PMID:11463916
 A;Accession: D95124
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-441 <XUR>
 A;Cross-references: UNIPROT:Q97QX1; UNIPARC:UPI00000516CB; GB:AB005672; PTDN:AAK75189.1;
 A;Experimental source: strain TIGR4
 C;Genetic:
 A;Gene: SP1076

```

Query Match          53.3%; Score 40; DB 2; length 441;
Best Local Similarity 53.8%; Pred. No. 51; 2; Indels 0; Gaps 0;
Matches 7; Conservative 4; Mismatches 2;
Oy          1 KGGRNLKSTRRQ 13
Db          416 KGSRMLKASKTQ 428

RESULT 11
P97994
Conserved hypothetical protein spr0982 [imported] - Streptococcus pneumoniae (strain R6)
C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: P97994
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E.Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McArdle, S.; McElroy, P.M.; Winkler, M.B.
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A.Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: P97994
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <KUR>
A;Cross-references: UNIPROT:Q8CWWR6; UNIPARC:UPI0000E493B; GB:AB007317; PIDN:AK99786.1;
C;Genetics:
A;Gene: spr0982

Query Match          53.3%; Score 40; DB 2; length 441;
Best Local Similarity 53.8%; Pred. No. 51; 2; Indels 0; Gaps 0;
Matches 7; Conservative 4; Mismatches 2;
Oy          1 KGGRNLKSTRRQ 13
Db          416 KGSRMLKASKTQ 428

RESULT 12
AG1431

```

C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AGI431
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusurgut, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001.
 A;Authors: Krefet, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AGI431
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-44 <GLA>
 A;Cross-references: UNIPROT:Q926Q3; UNIPARC:UPI00000555E0; GB:NC_003210; PIDN:CAD01069.1
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: rpmH
 C;Superfamily: Escherichia coli ribosomal protein L34
 Query Match 52.0%; Score 39; DB 2; Length 44;
 Best Local Similarity 53.3%; Pred. No. 9.3%;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 25 KNGRRVLASRRRKG 39
 RESULT 13
 AEL805
 ribosomal protein L34 [imported] - Listeria innocua (strain Clp11262)
 C;Species: Listeria innocua
 C;Accession: AE1805
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusurgut, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001.
 A;Authors: Krefet, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1077
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-44 <GLA>
 A;Cross-references: UNIPROT:Q926Q3; UNIPARC:UPI00000555E0; GB:AL592022; PIDN:CAC98213.1;
 A;Experimental source: strain Clp11262
 C;Genetics:
 A;Gene: rpmH
 C;Superfamily: Escherichia coli ribosomal protein L34
 Query Match 52.0%; Score 39; DB 2; Length 44;
 Best Local Similarity 53.3%; Pred. No. 9.3%;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 25 KNGRRVLASRRRKG 39
 RESULT 14
 S56117
 spermid-specific protein T2 precursor - longfin squid
 N;Alternate names: sperm protein SP
 C;Species: Loligo paucim (longfin squid)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S56117
 R;Wouters-Tyrou, D.; Martin-Ponchon, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; Bioc'h, J. 309, 520-534, 1995
 A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protam

A;Reference number: S56116; MUID:95351983; PMID:7626016
 A;Accession: S56117
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-118 <WOL>
 A;Cross-references: UNIPROT:Q7M4A3; UNIPARC:UPI00017BDD7
 Query Match 52.0%; Score 39; DB 2; Length 118;
 Best Local Similarity 50.0%; Pred. No. 23%;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 14
 Db 19 KGGRRRRRSRRR 32
 RESULT 15
 T24499
 hypothetical protein T05A6.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Thomas, K.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: Z19899
 A;Accession: T24499
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-258 <WIL>
 A;Cross-references: UNIPROT:Q22198; UNIPARC:UPI000007A24C; EMBL:Z50796; PIDN:CAA90670.1;
 A;Experimental source: clone T05A6
 C;Genetics:
 A;Gene: CESP-T05A6.2
 A;Map position: 2
 A;Introns: 25/3; 134/2; 157/1; 211/2
 Query Match 52.0%; Score 39; DB 2; Length 258;
 Best Local Similarity 66.7%; Pred. No. 46%;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KGGRKMLKSTRQR 15
 Db 240 KRMMLKSTRRSRR 251
 Search completed: February 4, 2006, 03:42:21
 Job time : 29.333 secs

GenCore version 5.1.7
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On protein - protein search, using SW model
Run on: February 4, 2006, 03:26:53 ; Search time 169.444 Seconds
Maximum DB seq length: 0 (without alignments)
Post-processing: Minimum Match 0%
Database : Maximum Match 100%
listing first 45 summaries

Title: US-10-790-768A-2
Perfect score: 75
Sequence: 1 KGGRKMLKSTRRR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 0 (without alignments)

Post-processing: Minimum Match 0%

Database : Maximum Match 100%

listing first 45 summaries

Database : UniProt_05_80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	62.7	406	2 Q5R212_RAT	Q5R212 rat
2	45	60.0	432	2 Q7UBK9_SYNPK	Q7UBK9 synaptochrome
3	44	58.7	32	2 QNDY79_MMC	QNDY79 arthropo
4	44	58.7	33	2 O6AAK0_PR0AC	O6AAK0 proline
5	44	58.7	77	1 PRT2_SEP0F	PRT2; SEP0F
6	44	58.7	78	1 PRT1_SEP0F	PRT1; SEP0F
7	44	58.7	78	2 Q86C60_LOL0P	Q86C60 loligo opal
8	44	58.7	79	2 Q7M4G6_LOL0P	Q7M4G6 loligo peal
9	44	58.7	173	2 Q84RV6_ORVSA	Q84RV6 oryza sativ
10	44	58.7	409	2 Q8CD06_MOUSE	Q8CD06 mus musculu
11	44	58.7	409	2 Q8C0F9_MOUSE	Q8C0F9 mus musculu
12	44	58.7	409	2 Q8C0L2_MOUSE	Q8C0L2 mus musculu
13	44	58.7	773	2 Q7ZLJ1_ANOGA	Q7ZLJ1 anophales g
14	43	57.3	32	2 Q9WKO7_STRCO	Q9WKO7 streptomyce
15	43	57.3	33	2 Q4JSX2_CORBP	Q4JSX2 cornebacter
16	43	57.3	33	2 Q8PSG0_COBPP	Q8PSG0 corynebacter
17	43	57.3	33	2 Q8NT55_CORG1	Q8NT55 corynebacte
18	43	57.3	44	1 RL34_THEMEA	RL34 themeata
19	43	57.3	44	2 Q4TQ78_9SPHN	Q4TQ78 erythroblast
20	43	57.3	114	2 Q5JUN6_CANVAL	Q5JUN6 candida alb
21	43	57.3	138	2 Q62IR5_ORVSA	Q62IR5 oryza sativ
22	43	57.3	175	2 Q4SSY8_TEETING	Q4SSY8 tetradon
23	43	57.3	282	2 Q8LMHO_ORVSA	Q8LMHO oryza sativ
24	43	57.3	386	2 Q8SL12_ORVSA	Q8SL12 oryza sativ
25	43	57.3	892	2 Q4QAJ7_LEIMA	Q4QAJ7 leishmania
26	42	56.0	68	1 HSP1_TACAC	HSP1 tachyglobu
27	42	56.0	131	2 Q5V3T7_MOUSE	Q5V3T7 mus muscu
28	42	56.0	191	2 Q5V3J3_BRAR8	Q5V3J3 brachydio
29	42	56.0	199	1 HEM4_PROMI	HEM4 proteo mir
30	42	56.0	241	2 Q7R3H5_GIADA	Q7R3H5 giardia lam
31	42	56.0	262	2 Q6RSF3_HPB0U	Q6RSF3 duck hepati

ALIGNMENTS

32	42	56.0	305	2 Q6RSF4_HBBDU	Q6RSF4 duck hepati
33	42	56.0	322	2 Q4KIC6_PBEFS	Q4KIC6 pseudomonas
34	42	56.0	300	2 Q13303_CRYCU	Q13303 cryptococcu
35	42	56.0	516	2 Q4ZRHS_TETING	Q4ZRHS tetradoon n
36	42	56.0	608	2 Q8BK43_MOUSE	Q8BK43 m mus muscu
37	42	56.0	669	2 Q5ACY9_CANAL	Q5ACY9 candida alb
38	42	56.0	700	2 Q6FVZ7_CANGA	Q6FVZ7 candida gla
39	42	56.0	708	2 Q963H4_HUMAN	Q963H4 homo sapien
40	41	54.7	45	1 QK34_GRAUTL	Q6951 gracilaria
41	41	54.7	125	2 Q8FH66_ECOL16	Q8FH66 escherichia
42	41	54.7	137	2 Q4NW87_98BLT	Q4NW87 anaeromyxob
43	41	54.7	167	2 Q69K45_ORVSA	Q69K45 oryza sativ
44	41	54.7	214	2 Q84ZK3_ORVSA	Q84ZK3 oryza sativ
45	41	54.7	276	2 Q89FA1_BRAYJA	Q89FA1 bradyrhizob

1	1	1	1	1	1
2	2	2	2	2	2
3	3	3	3	3	3
4	4	4	4	4	4
5	5	5	5	5	5
6	6	6	6	6	6
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25	25	25	25	25	25
26	26	26	26	26	26
27	27	27	27	27	27
28	28	28	28	28	28
29	29	29	29	29	29
30	30	30	30	30	30
31	31	31	31	31	31

RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
 RA Chain P., Lamerdin J.E., Regala W., Allen E.B., McCarron J.,
 RA Paulsen I.T., Durkin A., Partensky F., Webb R.A., Waterbury J.;
 RT "The genome of a motile marine cyanobacterium, *Synechococcus*."
 RL -1- SIMILARITY: Contains 1 PDZ (DHR) domain.
 CC DR -1- PROTEIN: BX569650; CAB07123.1; -; Genomic DNA.
 DR GO; GO:0008233; P-peptidase activity; IEA.
 DR GO; GO:0005515; P-protein binding; IEA.
 DR GO; GO:0004235; P-trypsin activity; IEA.
 DR GO; GO:0006508; P-proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001940; Peptidase_SIC.
 DR InterPro; IPR001524; Peptidase_SI_S6.
 DR Pfam; PF00059; PDZ; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00334; PROTEASESIC.
 DR SMART; SNO0228; PDZ; 1.
 DR SMART; SNO0020; Tryp_Spc; 1.
 DR PROSITE; PS50106; PDZ; 1.
 KW Complete proteome; Hydrolase; Protease; Serine protease; signal.
 FT SIGNAL
 SEQUENCE 432 AA; 46789 MW; 918E34B0CDF1942E CRC64;
 SQ Q4NDY7 8M1CC
 ID Q4NDY7_9M1CC PRELIMINARY; PRT; 32 AA.
 AC Q4NDY7;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=Arthrobacter_1453;
 OS Arthrobacter sp. FB24.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; Arthrobacter.
 OX NCBI_TAXID=290399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 STRAIN=FB24;
 RC US DOE Joint Genome Institute (JGI-PGFI);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammow N., Israeli S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.;"
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RG NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24;
 RG US DOE Joint Genome Institute (PGF-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.;"
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC preliminary data. EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; AAHG0100010; EAL95472.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 32 AA; 4083 MW; 3DFEAE9P6371E689 CRC64;
 Query Match 58.7%; Score 44; DB 2; Length 32;
 Best Local Similarity 60.0%; Pred. No. 2 2;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 1 KGGRKMLKSTRQR 14
 Db 13 KGGBLIKLKHRRQR 26

RESULT 3

Query Match 60.0%; Score 45; DB 2; Length 432;
 Best Local Similarity 64.3%; Pred. No. 24;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 1 KGGRKMLKSTRQR 14
 Db 13 KGGBLIKLKHRRQR 26

RESULT 4

Query Match 58.7%; Score 44; DB 2; Length 33;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 10; Conservative 1; Mismatches 1; Indels 4; Gaps 0;
 OY 1 KGGRKMLKSTRQR 15
 Db 15 KGHRLKLKTRIQR 29

RESULT 5

Query Match 58.7%; Score 44; DB 2; Length 33;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 10; Conservative 1; Mismatches 1; Indels 4; Gaps 0;
 OY 1 KGGRKMLKSTRQR 15
 Db 15 KGHRLKLKTRIQR 29

PROTEIN SEQUENCE OF 22-77.

PROTEIN SEQUENCE OF 22-77.

MEDLINE=9115398; PubMed=1999185;

"Cuttlefish sperm-specific protein T." Molecular characterization
 of two variants T1 and T2, putative precursors of sperm protamine
 variants Sp1 and Sp2." J. Biol. Chem. 266:17386-17395 (1991).

RN [2]

Wouters-Tyrou D., Charrier-Harlin M.-C., Martin-Ponthieu A.,
 Boutillon C., Van Dorsselaer A., Sautiere P.,
 RT "Cuttlefish sperm-specific protein T." Molecular characterization
 of two variants T1 and T2, putative precursors of sperm protamine
 variants Sp1 and Sp2." J. Biol. Chem. 266:17386-17395 (1991).

RN [2]

Wouters-Tyrou D., Charrier-Harlin M.-C., Martin-Ponthieu A.,
 Boutillon C., Van Dorsselaer A., Sautiere P.,
 RT "Cuttlefish sperm-specific protein T." Molecular characterization
 of two variants T1 and T2, putative precursors of sperm protamine
 variants Sp1 and Sp2." J. Biol. Chem. 266:17386-17395 (1991).

RN [2]

Wouters-Tyrou D., Charrier-Harlin M.-C., Martin-Ponthieu A.,
 Boutillon C., Van Dorsselaer A., Sautiere P.,
 RT "Cuttlefish sperm-specific protein T." Molecular characterization
 of two variants T1 and T2, putative precursors of sperm protamine
 variants Sp1 and Sp2." J. Biol. Chem. 266:17386-17395 (1991).

RN [2]

Bur. J. Biochem. 195:611-619 (1991).

CC -1- FUNCTION: Cuttlefish spermiogenesis is characterized by a double
 nuclear protein transition: histones -> spermatid-specific
 proteins (T1/T2) -> potamines (SP1/SP2). The proteins compact
 sperm DNA into a highly condensed, stable and inactive complex.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -|- TISSUE SPECIFICITY: Testis.
 CC -|- DEVELOPMENTAL STAGE: Spermatogenesis.
 CC -|- PTM: Phosphorylation occurs at different degrees. The triphosphorylated form may be predominant in T2. SP2 appears to be phosphorylated in elongated spermatids, but dephosphorylated in mature sperm cells.

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CC DR PIR; B40973; B40973.

CC KW Chromosomal protein; Developmental protein; Differentiation; Direct protein sequencing; DNA condensation; DNA-binding;

CC KW Multigene family; Nuclear protein; Nucleosome core; Phosphorylation; Spermatogenesis; Testis.

CC PT CHAIN 1 77 Spermid-specific Protein T2.

CC PT CHAIN 22 77 Sperm protamine SP2.

CC FT REGION 1 21 Hydrophobic.

CC PT COMBIAS 22 77 Arg-rich (highly basic).

CC PT VARIANT 1 1 Missing (in T2B).
 SQ SEQUENCE 77 AA; 10485 MW; 0FC1B21529280D7 CRC64;

Query Match 58.7%; Score 44; DB 1; Length 77;
 Best Local Similarity 53.3%; Pred. No. 5.7;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KGGRKMLKSTRQR 15
 ||||: : :|:
 Db 19 KGGRRRRRKSRRRR 33

RESULT 6

ID	PRT1_SEPOP	STANDARD:	PRT;	78 AA.
AC	P80001;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	01-MAY-2005 (Rel. 47, Last annotation update)			
DE	Spermaticid-specific protein TI [Contains: Sperm protamine SP1].			
OS	Sepia officinalis (Common cuttlefish).			
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;			
OX	NCBI_TAXID=6610;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RX	MEDLINE=9137359; PubMed=1894625;			
RA	Wouters-Tyrou D., Charlier-Harlin M.-C., Martin-Ponthieu A.,			
RA	Boutillon C., van Dorsselaer A., Sautiere P.,			
RT	"Cuttlefish spermatid-specific protein T. Molecular characterization of two variants Sp1 and Sp2".			
RT	J. Biol Chem. 266:17388-17395(1991).			
RL	[2]			
RN	PROTEIN SEQUENCE OF 22-78.			
RX	MEDLINE=91153298; PubMed=1999185;			
RA	Martin-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautiere P.,			
RA	"Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants." Eur. J. Biochem. 195:611-619(1991).			
RT	- - FUNCTION: Cuttlefish spermatogenesis is characterized by a double nuclear protein transition: histones -> spermatid-specific proteins (T1/T2) -> Protamines (SP1/SP2). The protamines compact sperm DNA into a highly condensed, stable and inactive complex.			
CC	- - SUBCELLULAR LOCATION: Nuclear.			
CC	- - TISSUE SPECIFICITY: Testis.			
CC	- - DEVELOPMENTAL STAGE: Spermatogenesis.			
CC	- - PTM: Phosphorylation occurs at different degrees. The triphosphorylated form may be predominant in T1. SP1 appears to be phosphorylated in elongated spermatids, but dephosphorylated in mature sperm cells.			

CC mature sperm cells.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR PIR; A40973; A40973.

CC KW Chromosomal protein; Developmental protein; Differentiation; Direct protein sequencing; DNA condensation; DNA-binding;

CC KW Multigene family; Nuclear protein; Nucleosome core; Phosphorylation; Spermatogenesis; Testis.

CC PT CHAIN 1 78 Spermid-specific protein T1.

CC PT CHAIN 22 78 Sperm protamine SP1.

CC FT REGION 1 21 Hydrophobic.

CC PT COMBIAS 22 78 Arg-rich (highly basic).

CC PT VARIANT 1 1 Missing (in T1).

SQ SEQUENCE 78 AA; 10632 MW; 09FB3EDBF0DCEB33 CRC64;

Query Match 58.7%; Score 44; DB 1; Length 78;
 Best Local Similarity 53.3%; Pred. No. 5.8;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KGGRKMLKSTRQR 15
 ||||: : :|:
 Db 19 KGGRRRRRKSRRRR 33

RESULT 7

ID	Q86G60	LOL0P	PRELIMINARY;	PRT;	78 AA.
AC	Q86G60;				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DB	Protamine.				
OS	Loigo opalescens (California market squid).				
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;				
OC	Decapodiformes; Sepiolidae; Sepiidae; Sepia.				
OX	NCBI_TAXID=31211;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	Published=15461424; DOI=10.1007/s00239-004-2589-8;				
RA	Levis J.D., de Jong M.E., Bagha S.M., Tang A., Gilly W.F., Ausio J.;				
RT	"All roads lead to arginine: the squid protamine gene.";				
RL	J. Mol. Evol. 58:673-680(2004).				
DR	EMBL: AV269798; AAP32169.1; -: Genomic DNA.				
SQ	SEQUENCE 78 AA; 10651 MW; FD446437AF1B3278 CRC64;				
Query Match 58.7%; Score 44; DB 2; Length 78; Best Local Similarity 53.3%; Pred. No. 5.8; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;					
Qy 1 KGGRKMLKSTRQR 15 : : : : Db 19 KGGRRRRRKSRRRR 33					

RESULT 8

ID	Q7M4G6	LOLPE	PRELIMINARY;	PRT;	79 AA.
AC	Q7M4G6;				
DT	01-MAR-2004 (TREMBLrel. 26, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DB	Spermid-specific protein T1.				
OS	Loigo opaleatus (longfin squid).				
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;				
OC	Decapodiformes; Loliginidae; Loigo.				
OX	NCBI_TAXID=6621;				
RN	[1]				
RP	PROTEIN SEQUENCE.				

RA Wouters-Tyrou D., Martin-Ponthieu A., Ledoux-Andula N., Kouach M.,
 RA Quinodo M., Subirana J.A., Sautiere P.;
 RT "Squid spermogenesis: molecular characterization of testis-specific
 RT pro-proteins";
 RL Biochem. J. 309:529-534(1995).
 RN [21]

RP PROTEIN SEQUENCE.

RL Biochem. J. 309 (Pt 2):529-534(1995).
 RX PubMed:7626016;
 RA Wouters-Tyrou D., Martin-Ponthieu A., Ledoux-Andula N., Kouach M.,
 RA Jaquinod M., Subirana J.A., Sautiere P.;
 RT "Squid spermogenesis: molecular characterization of testis-specific
 RT pro-proteins";
 RL Biochem. J. 309 (Pt 2):529-534(1995).
 DR PIR: 556116; S56116;
 RA SEQUENCE 79 AA; 10788 MW; 700CBED7397E42A CRC64;

Query Match 58.7%; Score 44; DB 2; Length 79;
 Best local Similarity 53.3%; Pred. No. 5.8;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KGGGRNLKSTRQR 15
 Db 19 KGGRRRRRRRRR 33

RESULT 9

Q84RV6 ORYSA

ID Q84RV6_ORYSA PRELIMINARY; PRT; 173 AA.

AC Q84RV6;

DT 01-JUN-2003 (TREMBLel. 24, Last sequence update)
 01-JUN-2003 (TREMBLel. 24, Created)

DT 01-MAR-2004 (TREMBLel. 26, Last annotation update)

DE HYPothetical protein P0571D04_112;
 Name=P0571D04_112;

GN

OS Oryza sativa (Japonica cultivar-group).

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

RN [1] _TaxID=39947;

RP NUCLEOTIDE SEQUENCE.

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
 clone: P0571D04_112";
 Submitted (NOV-2001) to the ENBL/GenBank/DBDJ databases.

DR EMBL: AP004315; BAD65921.1; -; Genomic_DNA.

DR Gramene: Q84RV6; -;

DR Hypothetical protein.

SQ SEQUENCE 173 AA; 18972 MW; 238484166673BB67 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 173;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KGGGRNLKSTRQR 15
 Db 36 KGGRRRRRRR 50

RESULT 10

Q8C06_MOUSE

ID Q8C06_MOUSE PRELIMINARY; PRT; 409 AA.

AC Q8C06;

DT 01-MAR-2003 (TREMBLel. 23, Created)
 01-MAR-2003 (TREMBLel. 23, Last sequence update)
 01-MAR-2004 (TREMBLel. 26, Last annotation update)

DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
 enriched library, clone:603046M24 product:similar to DJ223B3.1
 (PUTATIVE SECRETED PROTEIN ZSGI13), full insert sequence.

DE Name=PRB855;
 OS Mus musculus (Mouse).
 Buksyota; Metzoco; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OK NEBI_TAXID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RL Carninci P., Hayashiaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 Meth. Enzymol. 303:19-44(1999).
 RN [21]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RL MEDLINE=21055660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Mizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Asahineri M., Batyalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons J., Marchionni L., Mashima J., Mazzaferri J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka H., Wang K.H., Witz C., Whitaker C., Wilming L.,
 RA Wrayshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RL MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Suganura Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RT Genome Res. 10:1617-1630(2000).
 RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RL MEDLINE=20530913; PubMed=11776861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Azuawa K., Nagatani S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitajima T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii J., Nakamura S., Hazama M., Nishihira T., Harada K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
 RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 84 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RT Sequencing pipeline with 84 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa N., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiwa S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AK031644, BAC27491.1; -, mRNA.
 DR MGII, MGII:2444800; PR9835.
 DR GO:0005615; C_extracellular_space; TAS.
 DR InterPro, IPR001254; Peptidase_S1_S6.
 DR PTAN, PR00089; Trypsin; I.
 DR SMART, SM00020; TRYPSIN; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 409 AA; 45736 MW; EC09B91E6800719C CRC64;
 Query Match 58.7%; Score 44; DB 2; Length 409;
 Best Local Similarity 53.3%; Pred. No. 34;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KGGRKMLKSTRROR 15
 Db 194 KGGRKRRGSKRSRR 208
 RESULT 11
 ID QBC0F9_MOUSE PRELIMINARY; PRT; 409 AA.
 AC QBC0F9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
 enriched library, clone:6030424122 product similar to DJR231E3.1
 (PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence (Protease,
 DE serine, 35);
 Name=PR835;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE:99205253; PubMed=1049636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 30:19-41(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE:2105660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawaji J., Shinagawa A., Shibata K., Yoshihino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kyobawa H., Kondo S., Yamamoto T.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Battalov S., Cabavant T.,
 RA Fleischmann W., Gasserland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matuo Y., Nakaido T., Pesole G., Quackenbush J.,
 RA Schirmer L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Saito K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blke J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Guatincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Masimla J., Mazzarrelli J., Mombartt P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shitara Y., Storch K.-F.,
 RA Suzuki H., Toyoko K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE:2235463; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osojo N., Saito R., Suzuki H., Yamamoto T., Kyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.B., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kaspin A., Matsuda H., Battalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla B., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glaszi C., Gozlik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurcockin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavani W.J., Peretea G., Pesole G.,
 RA Petrovsky N., Pilai R., Pontius J.U., Qi Z., Ramachandran S.,
 RA Ravasi T., Reed D.J., Reed J., Reid J., Ring B.Z., Rinewald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanebe Y., Wells C.,
 RA Wilming L.G., Wyntshaw-Boris A., Yanagisawa M., Yang I., Wang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane K., Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Isihi Y., Itoh M., Kawada I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yosinoo M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length DNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE:2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RT Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE:20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sakai N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsunai T., Tachiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishina T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watachiki M.,
 RA Yoneda Y., Ishikawa T., Ogawa M., Ohara J., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequencing pipeline for analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Carninci P., Arakawa T., Bono H., Hayashizaki Y.,
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Hayashizaki Y.,
 RA Fukuda S., Furuno M., Hanagata T., Hara A., Hayashizumi W.,
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Hayashizumi Y.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirayama T., Hirozane T.,
 RA Horii H., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kacoh H., Kohji Y., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai S., Sakamoto N., Samo H.,
 RA Sasaki D., Shiba K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Eye;

- RA MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899; RX

RA Strausberg R.L., Feinberg E.A., Grouse L.H., Derge J.G., Schuler G.D., RX

RA Krahnauer R.D., Collins F.S., Wagner L., Shemesh C.M., Schueler G.D., RX

RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., RX

RA Hinckley R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., RX

RA Diatchenko L., Matsunaga A., Moore T., Max S.I., Wang J.J., Hsieh F., RX

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RX

RA Brownstein M.J., Usdin T.B., Toshikoshi S., Carninci P., Prange C., RX

RA Brownstein M.J., Usdin T.B., Toshikoshi S., Carninci P., Prange C., RX

RA Carninci P., Logueillo N.A., Petersen G.J., Abramson R.D., Millany S.J., RX

RA Boase S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H., RX

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RX

RA Villalobos D.K., Musny D.M., Sodergren E.J., Liu X., Gibbs R.A., RX

RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RX

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RX

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RX

RA Rodriguez A.C., Grimwood J., Schnitz J., Meyer R.M., RX

RA Butterfield S.E., Krzyniawski M.J., Skalska U., Smialius D.E., RX

RA Schinner A., Schein J.E., Jones S.J.M., Marca M.A.; Madan A., RX

RA "Generation and initial analysis of more than 15,000 full-length human RX

RT and mouse cDNA sequences.;" RT

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). RT

[8]

RN [18]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Eye;

RA Strausberg R.; RX

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. RX

DR EMBL; AK031411; BAC27392.1; -; mRNA.

DR EMBL; BC075675; AAH75675.1; -; mRNA.

DR Ensemble; ENSMUSG0000033491; Mus musculus.

DR MGI; MGI:244800; PRB35.

DR GO: GO:0005615; C:extracellular space; TAS.

DR InterPro; IPR001254; Peptidase_S1_S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR PRINTS; PR0072.

DR SMART; SM00020; TRYPSIN.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR Hydrolase; Protease; Serine protease.

SQ 409 AA; 45787 MW; 6E2D4A908E7BF05 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 409; RX

Best Local Similarity 53.3%; Pred. No. 34; RX

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0; RX

QY 1 KGGGRNKKRRRQQ 15 RX

Db 194 KGGRKRRGSKRSR 208 RX

RESULT 12

Q8C015 MOUSE

AC Q8C015_MOUSE PRELIMINARY; PRT; 409 AA.

AC Q8C015; RX

DT 01-MAR-2003 (TREMBREL. 23, Created)

DT 01-MAR-2003 (TREMBREL. 23, Last sequence update)

DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)

DE Mus musculus 6 days neonate head cDNA. RIKEN full-length enriched library, clone:54301704 product similar to DJ223E3.1 (PUTATIVE SECRETED PROTEIN 2SIG13), full insert sequence.

GN Name=Prb835;

OS Mus musculus (Mouse)

OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; OC

OC Muridae; Muridae; Mus. OC

NCBI_TaxID=10909; [1]

RC NUCLEOTIDE SEQUENCE.

RA MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; RX

RA Carninci P., Hayashizaki Y.; RX

RT "High-efficiency full-length cDNA cloning.;" RT

RT Meth. Enzymol. 303:19-44(1999). RT

RN [12]

RP NUCLEOTIDE SEQUENCE.

DR InterPro: IPR001314; Peptidase_S1A.
 DR PRINTS: PR00722; CHIMOTRIPSIN.
 DR SMART: SM00020; TRYSP_CPC_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE: 409 AA; 45847 MW; ASAC1C582BFD352E CRC64;
 RESULT 13
 07PZL1 AMOGA
 ID 07PZL1 AMOGA PRELIMINARY; PRT; 773 AA.
 AC 07PZL1;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENSANGP0000008690 (Fragment).
 GN ORFnames=ENSAHG000000546;
 OS Anopheles gambiae Str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anopheline; Anopheles.
 OX NCBI_TAXID:180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG "The Anopheles gambiae Sequence Committee";
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG "The Anopheles gambiae Sequence Committee";
 RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RL [1]
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR GO: GO:0005241; F-ATP binding; IEA.
 DR InterPro: IPR003955; AMP_ATPase_centr.
 DR Pfam: PF00004; AAA_1.
 DR Pfam: PF00612; IQ_1.
 KW ATP-binding; Nucleotide-binding.
 PT NON_TER 1
 PT SEQUENCE 773 AA; 89340 MW; 5B6781DCFF48C2784 CRC64;
 SQ
 Query Match 58.7%; Score 44; DB 2; Length 773;
 Best local Similarity 46.7%; Pred. No. 67;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGGRKMLKSTRQR 15
 DB 427 RGGKIKLKKSSKARR 441
 RESULT 14
 Q9WQ07 STRCO
 ID Q9WQ07; STRCO PRELIMINARY; PRT; 32 AA.
 AC Q9WQ07;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein SCO3327.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A3(2); M145;
 RG "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)." ;
 DT Nature 417:141-147 (2002).
 DR EMBL: AL039115; CAB45361.1; -; Genomic_DNA.
 DR PIR: T36275; T36275.
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 32 AA; 4045 MW; 3DE18FA26371F5A9 CRC64;
 SQ
 Query Match 57.3%; Score 43; DB 2; Length 32;
 Best Local Similarity 66.7%; Pred. No. 3.4;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 1 KGGRKMLKSTRQR 15
 DB 15 KGGRKMLKSTRQR 29
 RESULT 15
 Q4JSX2 CORJK
 ID Q4JSX2 CORJK PRELIMINARY; PRT; 33 AA.
 AC Q4JSX2;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SBP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SBP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFnames=Jk1904;
 OS Corynebacterium jeikeium (strain K411).
 OC Bacteria; Actinobacteria; Actinomycetaleib; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TAXID:306537;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K411;
 DR PubMed:15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
 RA Tauch A., Kaiser O., Rain T., Goessmann A., Weisshaar B., Chakrabarty T.,
 RA Albersmeier A., Kaiser O., Rain T., Goessmann A., Weisshaar B., Chakrabarty T.,
 RA Kalinowski J., Meyer F., Rupp O., Schneiker S., Vinkenover P.,
 RA Puiller A.;
 RT "Complete Genome Sequence and Analysis of the Multiresistant
 Nosocomial Pathogen Corynebacterium Jeikeium K411, a Lipid-Requiring
 Bacterium of the Human Skin Flora.", J. Bacteriol. 187:4671-4682 (2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K411;
 RA Linker B.; Tauch A.;
 RL Submitted (DNC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CB931987; CAI38085.1; -; Genomic_DNA.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 33 AA; 4163 MW; 8156A587F163D4F5 CRC64;
 Query Match 57.3%; Score 43; DB 2; Length 33;
 Best Local Similarity 66.7%; Pred. No. 3.5;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Mon Feb 6 10:11:05 2006

us-10-790-768a-2.rup

Page 8

Qy 1 KGGKMLKSTRQR 15
| ||| : ||||| 29
15 KKHKKMLRRTVOR 29

Search completed: February 4, 2006, 03:41:26
Job time : 170.444 SECs

GenCore version 5.1.7
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OM protein - protein search, using SW model
Run on: February 4, 2006, 03:41:44 ; Search time 38.3333 Seconds
Sequence: 32.351 Million cell updates/sec

Title: US-10-790-768A-2
Perfect score: 75
Sequence: 1 KGGRKMLKSTRRQRR 15

Scoring table: BLOSUM2
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata//1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata//1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata//1/1aa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RB_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	43	57.3	33	2 US-09-605-703B-2766 Sequence 2766, AP
2	42	56.0	174	2 US-09-107-532A-4569 Sequence 369, AP
3	42	56.0	249	2 US-09-543-611A-4404 Sequence 4404, AP
4	42	56.0	537	2 US-09-252-991A-25958 Sequence 25958, AP
5	41	54.7	413	2 US-09-993-833A-296 Sequence 296, AP
6	41	54.7	660	2 US-09-252-991A-22842 Sequence 22842, AP
7	41	54.7	725	2 US-09-252-991A-23752 Sequence 23752, AP
8	41	54.0	204	2 US-09-252-991A-27153 Sequence 27153, AP
9	40.5	53.3	160	2 US-09-134-001C-3904 Sequence 3904, AP
10	40	53.3	357	2 US-09-538-092-254 Sequence 254, AP
11	40	53.3	408	2 US-09-52-991A-32828 Sequence 32828, AP
12	40	53.3	441	2 US-09-583-110-3763 Sequence 3763, AP
13	40	53.3	442	2 US-09-107-43-4820 Sequence 4820, AP
14	40	53.3	442	2 US-09-107-43-4820 Sequence 445, AP
15	39	52.0	85	2 US-09-107-433-4454 Sequence 8105, AP
16	39	52.0	131	2 US-09-51-999C-8105 Sequence 8105, AP
17	39	52.0	277	2 US-09-243-796A-16606 Sequence 16606, AP
18	39	52.0	1291	2 US-09-52-991A-19504 Sequence 19504, AP
19	38	50.7	247	2 US-09-902-54-0-10732 Sequence 10732, AP
20	38	50.7	305	2 US-09-241-58-11 Sequence 11, AP
21	38	50.7	312	2 US-09-134-001C-3669 Sequence 3669, AP
22	38	50.7	404	2 US-09-252-991A-25830 Sequence 25830, AP
23	38	50.7	494	2 US-09-252-991A-28162 Sequence 28162, AP
24	37	49.3	44	2 US-09-732-21-933 Sequence 933, AP
25	37	49.3	44	2 US-09-733-21-945 Sequence 945, AP
26	37	49.3	48	2 US-09-733-21-948 Sequence 948, AP
27	37	49.3	147	2 US-09-252-991A-29687 Sequence 29687, AP

RESULT 1
US-09-605-703B-2766
; Sequence 2766, Application US/09605703B
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL FILE REFERENCE: BGI-129C
CURRENT APPLICATION NUMBER: US/09/605, 703B
CURRENT FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: 601142, 764
PRIORITY FILING DATE: 1999-07-08
PRIORITY APPLICATION NUMBER: 601512, 318
NUMBER OF SBQ ID NOS: 2934
SBQ ID NO: 2766
; LENGTH: 33
; SEQ ID NO: 2766
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2766
Query Match Score 57.3%; Pred. No. 2.3;
Best Local Similarity 66.7%; Mismatches 4;
Matches 10; Conservative 1; Indels 0; Gaps 0;
Ov 1 KGGRKMLKSTRRQRR 15
Db 15 KGGRKMLKSTRRQRR 29

ALIGNMENTS

Sequence 7013, AP
Sequence 4569, AP
Sequence 27, AP
Sequence 27, AP
Sequence 6589, AP
Sequence 8739, AP
Sequence 2014, A
Sequence 3220, A
Sequence 2, APPL
Sequence 2, APPL
Sequence 2714, A
Sequence 2857, A
Sequence 5655, AP
Sequence 4511, AP
Sequence 2573, A
Sequence 2853, A
Sequence 1723, A
Sequence 3, APPL

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADRESSEUR: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA

ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 3699:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..174
 SEQUENCE DESCRIPTION: SEQ ID NO: 3699:
 US-09-107-532A-3699

Query Match 56 0%; Score 42; DB 2; Length 174;
 Best Local Similarity 57.1%; Pred. No. 16;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGKMKLKSRRQR 15
 Db 7 GGRKMKIKAVRIDER 20

RESULT³
 US-09-543-681A-4404
 ; Sequence 4404, Application US/09543681A.
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709_1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 4404
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 ; US-09-543-681A-4404

Query Match 56.0%; Score 42; DB 2; Length 248;
 Best Local Similarity 61.5%; Pred. No. 23;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGKMKLKSRRQR 14
 Db 139 GGRELATTIQR 151

RESULT⁴
 US-09-252-991A-25958
 ; Sequence 25958, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107195-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25958
 ; LENGTH: 537
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-25958

Query Match 56.0%; Score 42; DB 2; Length 537;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGKMKLKSRRQR 15
 Db 400 GSRLURRQRRRR 413

RESULT⁵
 US-09-999-833A-296
 ; Sequence 296, Application US/09999833A
 ; Patent No. 6916848
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Denoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanpeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kijavim, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tunas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William T.

Query Match 56.0%; Score 42; DB 2; Length 248;
 Title of Invention: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 File Reference: P2630P1C5
 Current Application Number: US/09/999,833A
 Current Filing Date: 2001-10-24
 Prior Application Number: 09/918585
 Prior Filing Date: 2001-07-30
 Prior Application Number: 60/062250
 Prior Filing Date: 1997-10-17

PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077532
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077532
PRIOR APPLICATION NUMBER: 60/085589	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/085573	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/077791	PRIOR APPLICATION NUMBER: 60/077791
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PRIOR APPLICATION NUMBER: 60/085573	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/078886
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/078936	PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/085697	PRIOR FILING DATE: 1998-05-20	PRIOR APPLICATION NUMBER: 60/078936
Query Match	54.7%	Score 41; DB 2; Length 413;
Best Local Similarity	54.7%	Pred. No. 53;
Sequence 296, Application US/10020445A	Matches 9;	Mismatches 4;
Patent No. 6962797	Indels 0;	Gaps 0;
GENERAL INFORMATION:		
APPLICANT: Abkenazi, Avi		
APPLICANT: Baker, Kevin P.		
APPLICANT: Botstein, David		
APPLICANT: Desnoyers, Luc		
APPLICANT: Eaton, Dan		
APPLICANT: Ferrara, Napoleon		
APPLICANT: Filvaroff, Ellen		
APPLICANT: Fong, Sherman		
APPLICANT: Gao, Wei-Qiang		
APPLICANT: Gerber, Hanspeter		
APPLICANT: Gerritsen, Mary E.		
APPLICANT: Goddard, Audrey		
APPLICANT: Grimaldi, J. Christopher		
APPLICANT: Gurney, Austin L.		
APPLICANT: Hillan, Kenneth J		
APPLICANT: Kljavin, Ivar J.		
APPLICANT: Kuo, Sophia S.		
APPLICANT: Napier, Mary A.		
APPLICANT: Pan, James		
APPLICANT: Paoni, Nicholas F.		
APPLICANT: Roy, Margaret Ann		
APPLICANT: Sheldon, David L.		
APPLICANT: Stewart, Timothy A.		
APPLICANT: Tumas, Daniel		
APPLICANT: Williams, P. Mickey		
APPLICANT: Wood, William I.		
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
FILE REFERENCE: P26301C74		
CURRENT APPLICATION NUMBER: US/10/020445A		
CURRENT FILING DATE: 2001-04-24		
PRIOR APPLICATION NUMBER: 60/918585		
PRIOR FILING DATE: 2001-07-30		
PRIOR APPLICATION NUMBER: 60/062250		
PRIOR FILING DATE: 1997-10-17		
PRIOR APPLICATION NUMBER: 60/064249		
PRIOR FILING DATE: 1997-11-03		
PRIOR APPLICATION NUMBER: 60/065311		
PRIOR FILING DATE: 1997-11-13		
PRIOR APPLICATION NUMBER: 60/066364		
PRIOR FILING DATE: 1997-11-21		
PRIOR APPLICATION NUMBER: 60/077450		

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; PROR APPLICATION NUMBER: 60/081838
; PROR FILING DATE: 1998-04-15
; PROR APPLICATION NUMBER: 60/082268
; PROR FILING DATE: 1998-04-21
; PROR APPLICATION NUMBER: 60/082569
; PROR FILING DATE: 1998-04-21
; PROR APPLICATION NUMBER: 60/082704
; PROR FILING DATE: 1998-04-22
; PROR APPLICATION NUMBER: 60/082804
; PROR FILING DATE: 1998-04-22
; PROR APPLICATION NUMBER: 60/082700
; PROR FILING DATE: 1998-04-22
; PROR APPLICATION NUMBER: 60/083336
; PROR FILING DATE: 1998-04-27
; PROR APPLICATION NUMBER: 60/083322
; PROR FILING DATE: 1998-04-28
; PROR APPLICATION NUMBER: 60/083392
; PROR FILING DATE: 1998-04-29
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; PROR FILING DATE: 1998-04-29
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; PROR APPLICATION NUMBER: 60/083499
; PROR FILING DATE: 1998-04-29
; PROR APPLICATION NUMBER: 60/083545
; PROR FILING DATE: 1998-04-29
; PROR APPLICATION NUMBER: 60/083554
; PROR FILING DATE: 1998-04-29
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; PROR APPLICATION NUMBER: 60/083500
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; PROR APPLICATION NUMBER: 60/084643
; PROR FILING DATE: 1998-05-07
; PROR APPLICATION NUMBER: 60/085339
; PROR FILING DATE: 1998-05-13
; PROR APPLICATION NUMBER: 60/085338
; PROR FILING DATE: 1998-05-13
; PROR APPLICATION NUMBER: 60/085323
; PROR FILING DATE: 1998-05-13
; PROR APPLICATION NUMBER: 60/085582
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085700
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085689
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085579

; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085580
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085573
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085704
; PROR FILING DATE: 1998-05-15
; PROR APPLICATION NUMBER: 60/085697

RESULT 7
US-09-252-991A-22842
; Sequence 22842, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196_136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22842
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

RESULT 8
US-09-252-991A-23752
; Sequence 23752, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 10716_136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23752
; LENGTH: 725
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

Query Match 54.7%; Score 41; DB 2; Length 413;
Best Local Similarity 64.3%; Pred. No. 53; Mismatches 4; Indels 0; Gaps 0;
Matches 9; Conservative 1; MisMatches 4; Indels 0; Gaps 0;

Qy 1 KGGRMLKSTRQR 14
Db 228 KGGRRKUSGRGQR 241

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RESULT 9
 US-09-252-991A-27153
 ; Sequence 27153 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 27153
 ; LENGTH: 204
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-27153

Query Match 54.0%; Score 40; DB 2; Length 204;
 Best Local Similarity 55.2%; Pred. No. 33; Mismatches 9; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 KGGRK-MLAISTRRRR 15
 Db 184 RGGRGVAASTRRAK 199

RESULT 10
 US-09-134-001C-3904
 ; Sequence 3904, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 3904
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3904

Query Match 53.3%; Score 40; DB 2; Length 160;
 Best Local Similarity 53.8%; Pred. No. 32; Mismatches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KGGRKMLKSTRRQ 13
 Db 3 RGGTKLKVLPTRRQ 15

RESULT 11
 US-09-538-092-254
 ; Sequence 254, Application US/09538092
 ; Patent No. 6753314

RESULT 12
 US-09-252-991A-32828
 ; Sequence 32828, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 32828
 ; LENGTH: 408
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-32828

Query Match 53.3%; Score 40; DB 2; Length 408;
 Best Local Similarity 50.0%; Pred. No. 76; Mismatches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGRKMLKSTRRR 15
 Db 87 GGQRRLRRRRRR 100

RESULT 13
 US-09-583-110-3763
 ; Sequence 3763, Application US/09583110
 ; Patent No. 6699703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553
 PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO 3763
 LENGTH: 441
 TYPE: PRT
 ORGANISM: *Streptococcus pneumoniae*
 US-09-533-110-3763

Query Match 53.3%; Score 40; DB 2; Length 441;
 Best Local Similarity 53.8%; Pred. No. 82;
 Matches 7; Conservative 4; Mismatches 2;
 Qy 1 KGGRKMLKSTRRQ 13
 Db 416 KGSRMLKASKTQ 428

RESULT 14
 US-09-107-433-4820
 Sequence 4820, Application US/09107433
 Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
 NUMBER OF SEQUENCES: 5206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Atinieillo, Pamela Deneka
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4454:
 SEQUENCE DESCRIPTION: SEQ ID NO: 4454:
 Query Match 52.0%; Score 39; DB 2; Length 85;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 3;
 Qy 1 KGGRKMLKSTRRQ 13
 Db 3 KGGNQMVTRKQ 15

RESULT 15
 US-09-107-433-4454
 Sequence 4454, Application US/09107433
 Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
 NUMBER OF SEQUENCES: 5206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Atinieillo, Pamela Deneka
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4454:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 85 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: *Streptococcus pneumoniae*
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1.. 85
 SEQUENCE DESCRIPTION: SEQ ID NO: 4454:
 US-09-107-433-4454

Query Match 52.0%; Score 39; DB 2; Length 85;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 3;
 Qy 1 KGGRKMLKSTRRQ 13
 Db 3 KGGNQMVTRKQ 15

SEARCH RESULTS
 INFORMATION FOR SEQ ID NO: 4820:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: *Streptococcus pneumoniae*
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1.. 442
 SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

Search completed: February 4, 2006, 03:43:34

Mon Feb 6 10:11:05 2006

us-10-790-768a-2.rai

Page 8

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OM protein - protein search, using BW model
 Run on: February 4, 2006, 03:42:34 ; Search time 130 Seconds
 (without alignments)
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Title: US-10-790-768A-2
 Perfect score: 75
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 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41782326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications AA Main:
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6: /cgn2_6_ptodata/1_pubpaa/us11_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	4 US-10-790-768A-2	Sequence 2, Appli
2	75	100.0	15	4 US-10-790-768A-14	Sequence 4, Appli
3	75	100.0	21	4 US-10-790-768A-4	Sequence 14, Appli
4	75	100.0	21	4 US-10-790-768A-19	Sequence 19, Appli
5	75	100.0	21	4 US-10-790-768A-20	Sequence 20, Appli
6	70	93.3	15	4 US-10-790-768A-16	Sequence 15, Appli
7	62	82.7	27	4 US-10-790-768A-5	Sequence 5, Appli
8	60	80.0	19	4 US-10-790-768A-18	Sequence 18, Appli
9	60	80.0	25	4 US-10-790-768A-21	Sequence 21, Appli
10	60	80.0	25	4 US-10-790-768A-22	Sequence 22, Appli
11	57.3	77.3	12	4 US-10-790-768A-1	Sequence 1, Appli
12	48	64.0	123	4 US-10-437-963-117103	Sequence 117103,
13	45	60.0	71	4 US-10-425-115-335780	Sequence 335780,
14	45	60.0	128	4 US-10-437-963-188683	Sequence 188683,
15	43	57.3	33	3 US-09-730-626-3964	Sequence 3964, Ap
16	43	57.3	247	4 US-10-408-765A-2219	Sequence 2219, Ap
17	43	57.3	282	4 US-10-437-963-122500	Sequence 122500,
18	42	56.0	145	4 US-10-424-599-276649	Sequence 276649,
19	42	56.0	708	4 US-10-408-765A-1772	Sequence 1772, Ap
20	41	54.7	153	4 US-10-425-115-225169	Sequence 225169,
21	41	54.7	155	4 US-10-425-115-347520	Sequence 347520,
22	41	54.7	413	3 US-09-888-615-89	Sequence 299, Ap
23	41	54.7	413	3 US-09-970-295-296	Sequence 296, Ap
24	41	54.7	413	3 US-09-970-697-296	Sequence 296, Ap
25	41	54.7	413	3 US-09-978-192A-296	Sequence 296, Ap
26	41	54.7	413	3 US-09-998-832A-296	Sequence 296, Ap
27	41	54.7	413	3 US-09-978-189-296	Sequence 296, Ap

ALIGNMENTS

RESULT 1
 US-10-790-768A-2
 ; Sequence 2, Application US/10790768A
 ; Publication No. US20040209797A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karas, Michael
 ; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
 ; Acids
 ; FILE REFERENCE: 002877.00028
 ; CURRENT APPLICATION NUMBER: US/10/790,768A
 ; CURRENT FILING DATE: 2004-03-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: protein transduction domain

```

NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Biotin
US-10-790-768A-14

RESULT 3
Query Match          100.0%; Score 75; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; SEQ ID NO: 4
Qy   1 KGGGRMLKSTRRQR 15
Db   1 KGGGRMLKSTRRQR 15

RESULT 4
Query Match          100.0%; Score 75; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; SEQ ID NO: 21
Qy   1 KGGGRMLKSTRRQR 15
Db   1 KGGGRMLKSTRRQR 15

RESULT 5
Query Match          100.0%; Score 75; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; SEQ ID NO: 20
Qy   1 KGGGRMLKSTRRQR 15
Db   1 KGGGRMLKSTRRQR 15

RESULT 6
Query Match          100.0%; Score 75; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; SEQ ID NO: 16
Qy   1 KGGGRMLKSTRRQR 15
Db   7 KGGGRMLKSTRRQR 21

RESULT 7
Query Match          93.3%; Score 70; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-05; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; SEQ ID NO: 19
Qy   1 KGGGRMLKSTRRQR 15
Db   1 KGGGRMLKSTRRQR 15

RESULT 8
Query Match          100.0%; Score 75; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; SEQ ID NO: 1
Qy   1 KGGGRMLKSTRRQR 15
Db   1 KGGGRMLKSTRRQR 15

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RESULT 7
US-10-790-768A-5
Sequence 5; Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790, 768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 27
TYPE: PRT
FEATURE: OTHER INFORMATION: protein transduction domain
ORGANISM: Artificial Sequence
US-10-790-768A-5

Query Match 82.7%; Score 62; DB 4; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.0037; 0; Mismatches 0; Indels 6; Gaps 1;
Matches 15; Conservative 0; Other 0; Location: (1..(1))
OTHER INFORMATION: protein transduction domain

RESULT 8
US-10-790-768A-18
Sequence 18; Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790, 768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 19
TYPE: PRT
FEATURE: OTHER INFORMATION: protein transduction domain
ORGANISM: Artificial Sequence
US-10-790-768A-18

Query Match 80.0%; Score 60; DB 4; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.0056; 0; Mismatches 0; Indels 4; Gaps 1;
Matches 14; Conservative 1; Other 0; Location: (1..(1))
OTHER INFORMATION: Biotin
US-10-790-768A-19

RESULT 9
US-10-790-768A-21
Sequence 21; Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790, 768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 27
TYPE: PRT
FEATURE: OTHER INFORMATION: protein transduction domain
ORGANISM: Artificial Sequence
US-10-790-768A-5

Query Match 80.0%; Score 60; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 0.0074; 0; Mismatches 0; Indels 4; Gaps 1;
Matches 14; Conservative 1; Other 0; Location: (1..(1))
OTHER INFORMATION: Biotin
US-10-790-768A-22

RESULT 10
US-10-790-768A-22
Sequence 22; Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790, 768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 25
TYPE: PRT
FEATURE: OTHER INFORMATION: protein transduction domain
ORGANISM: Artificial Sequence
US-10-790-768A-22

Query Match 80.0%; Score 60; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 0.0074; 0; Mismatches 0; Indels 4; Gaps 1;
Matches 14; Conservative 1; Other 0; Location: (1..(1))
OTHER INFORMATION: Biotin
US-10-790-768A-22

RESULT 11
US-10-790-768A-1
Sequence 1; Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790, 768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 1

LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: protein transduction domain
; US-10-790-768a-1

Query Match 77.3%; Score 58; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0075; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKMILKSTRRQR 15
Db 1 RKMILKSTRRQR 12

RESULT 12
Sequence 117103, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrej A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 117103
LENGTH: 123
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_20540C.1.pep
US-10-437-963-117103

Query Match 64.0%; Score 48; DB 4; Length 123;
Best Local Similarity 69.2%; Pred. No. 3.8; Mismatches 2; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KGGRKMLKSTRRQ 13
Db 11 KGGRKKEIRPPIRQ 23

RESULT 13
US-10-435-115-335780
Sequence 335780, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335780
LENGTH: 71
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_6933C.1.pep

US-10-425-115-335780
Query Match 60.0%; Score 45; DB 4; Length 71;
Best Local Similarity 64.3%; Pred. No. 12; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGRKMLKSTRRQR 15
Db 112 GGAKLAKSGRRRR 125

RESULT 15
US-09-738-626-3954
Sequence 3364, Application US/097388626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIJI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 243-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-11-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3964
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3964

Query Match 57.3%; Score 43; DB 3; Length 33;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGGKMLKSTRQR 15
Db 15 KGRKMLRTRVQR 29

Search completed: February 4, 2006, 03:47:34
Job time : 131 secB

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GenCore version 5.1.7

OM protein - protein search, using sw model
Run on: February 4, 2006, 03:43:49 ; Search time 10.5556 Seconds
16.652 Million cell updates/sec

Title: US-10-790-768a-2
Perfect score: 75

Sequence: 1 KGGRKMLKSTRQR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : Published Applications AA_New:*

1: /cgn2_6/podata/2/pubpaas/US08_NEW_PUB_pep:*

2: /cgn2_6/podata/2/pubpaas/US06_NEW_PUB_pep:*

3: /cgn2_6/podata/2/pubpaas/PCT_NEM_PUB_pep:*

4: /cgn2_6/podata/2/pubpaas/US05_NEW_PUB_pep:*

5: /cgn2_6/podata/2/pubpaas/US10_NEW_PUB_pep:*

6: /cgn2_6/podata/2/pubpaas/US11_NEW_PUB_pep:*

7: /cgn2_6/podata/2/pubpaas/US60_NEW_PUB_pep:*

8: /cgn2_6/podata/2/pubpaas/US60_NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	41	54.7	413	7 US-11-037-243-89
2	38	50.7	672	6 US-10-689-742-70
3	37	49.3	54	7 US-11-150-054A-13
4	37	49.3	54	7 US-11-150-054A-21
5	37	49.3	54	7 US-11-150-054A-26
6	36	48.0	154	6 US-10-821-234-1346
7	36	48.0	280	6 US-10-821-234-1300
8	35.5	47.3	327	7 US-11-165-211-52
9	35.5	47.3	327	7 US-11-165-226-62
10	35	46.7	342	6 US-10-714-887-10
11	35	46.7	441	7 US-11-024-959-10
12	35	46.7	844	6 US-10-453-372-852
13	35	46.7	844	6 US-10-453-372-856
14	34	45.3	356	6 US-10-161-408-50
15	34	45.3	543	7 US-11-169-041-162
16	33	44.0	441	7 US-11-024-959-280
17	33	44.0	441	7 US-11-024-959-281
18	33	44.0	521	7 US-11-091-914-2
19	33	44.0	663	7 US-11-024-959-314
20	33	44.0	860	7 US-11-019-711-59
21	32	42.7	99	6 US-10-467-657-5934
22	32	42.7	164	6 US-10-467-657-170
23	32	42.7	164	6 US-10-467-657-204
24	32	42.7	164	6 US-10-467-657-3632
25	32	42.7	164	6 US-10-467-657-6390

RESULT 1

US-11-037-243-89

; Sequence 89, Application US/11037243

; Publication No. US20050287546A1

; GENERAL INFORMATION:

; APPLICANT: PLOMMAN, GREGORY

; APPLICANT: WHYTE, DAVID

; APPLICANT: CAINEPPEL, SEAN

; APPLICANT: CHARVICKAK, GLEN

; APPLICANT: MANNING, GERARD

; APPLICANT: SUDARSANAM, SUCHA

; TITLE OF INVENTION: NOVEL PROTEASES

; FILE REFERENCE: 038602/1214

; CURRENT APPLICATION NUMBER: US11/037,243

; PRIOR APPLICATION NUMBER: US11/037,243

; PRIOR FILING DATE: 2005-05-26

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 89

; LENGTH: 413

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-037-243-89

Query Match

Best Local Similarity

54.7%; Score 41; DB 7; Length 413;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OQ ||||| | | | |

Db 228 KGGRKMLKSTRQR 241

ALIGNMENTS

Sequence 8516, App	Sequence 560, App
Sequence 273, App	Sequence 4, App
Sequence 8, App	Sequence 34, App
Sequence 214, App	Sequence 214, App
Sequence 159, App	Sequence 219, App
Sequence 22, App	Sequence 32, App
Sequence 11, App	Sequence 33, App
Sequence 62, App	Sequence 24, App
Sequence 146, App	Sequence 146, App
Sequence 892, App	Sequence 892, App

APPLICANT: Spaulding, Vicki
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 FILE REFERENCE: 00766_000091_10
 CURRENT APPLICATION NUMBER: US/10/689,742
 CURRENT FILING DATE: 2003-10-22
 PRIOR APPLICATION NUMBER: 09/746,783
 PRIOR FILING DATE: 2000-12-21
 NUMBER OF SEQ ID NOS: 231
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 70
 LENGTH: 672
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (107)..(107)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (645)..(645)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 LOCATION: (111)..(111)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (117)..(118)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (645)..(645)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-10-689-742-70

Query Match 50.7%; Score 38; DB 6; Length 672;
 Best Local Similarity 53.8%; Pred. No. 28; Mismatches 4; Indels 0; Gaps 0;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GRKMKMKSTRQR 15
 Db 597 GRKLEAGRRBSR 609

RESULT 3
 US-11-150-054A-13
 Sequence 13, Application US/11150054A
 Publication No. US20050278801A1
 GENERAL INFORMATION:
 APPLICANT: Lassner, Michael
 ATTORNEY: Wilkinson, Jack Q.
 TITLE OF INVENTION: Plastid Transit Peptides
 FILE REFERENCE: 2119-4284US1
 CURRENT APPLICATION NUMBER: US/11/150,054A
 CURRENT FILING DATE: 2005-06-09
 PRIOR APPLICATION NUMBER: 60/578,535
 NUMBER OF SEQ ID NOS: 57
 PRIOR FILING DATE: 2004-06-09
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 13
 LENGTH: 54
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptide
 US-11-150-054A-13

Query Match 49.3%; Score 37; DB 7; Length 54;
 Best Local Similarity 58.3%; Pred. No. 3..3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RPKMLKSTRQR 15
 Db 34 RRFNRRTRQR 45

RESULT 5
 US-11-150-054A-26
 Sequence 26, Application US/11150054A
 Publication No. US20050278801A1
 GENERAL INFORMATION:
 APPLICANT: Lassner, Michael
 ATTORNEY: Wilkinson, Jack Q.
 TITLE OF INVENTION: Plastid Transit Peptides
 FILE REFERENCE: 2119-4284US1
 CURRENT APPLICATION NUMBER: US/11/150,054A
 CURRENT FILING DATE: 2005-06-09
 PRIOR APPLICATION NUMBER: 60/578,535
 NUMBER OF SEQ ID NOS: 57
 PRIOR FILING DATE: 2004-06-09
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 26
 LENGTH: 54
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptide
 US-11-150-054A-26

Query Match 49.3%; Score 37; DB 7; Length 54;
 Best Local Similarity 58.3%; Pred. No. 3..3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RPKMLKSTRQR 15
 Db 34 RRFNRRTRQR 45

RESULT 6
 US-10-821-234-1344
 Sequence 1344, Application US/10821234
 Publication No. US2005025511A1
 GENERAL INFORMATION:
 APPLICANT: Habat, Ivan
 ATTORNEY: Stache-Crain, Birgit
 APPLICANT: Andamani, Susan
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

RESULT 4

```

FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO 1344
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1344

RESULT 7
US-10-821-234-1300
; Sequence Match 48.0%; Score 36; DB 6; Length 154;
; Best Local Similarity 57.1%; Pred. No. 14; Mismatches 3; Indels 0; Gaps 0;
; Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGRKMLKSTRRQR 15
Db 72 GGRKMLKSTRRQR 85

RESULT 8
US-10-821-234-1300
; Sequence Match 48.0%; Score 36; DB 6; Length 154;
; Best Local Similarity 50.0%; Pred. No. 26; Mismatches 4; Indels 0; Gaps 0;
; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GGRKMLKSTRRQR 15
Db 20 GGRKMLKSTRRQR 33

RESULT 9
US-11-165-226-62
; Sequence Match 47.3%; Score 35.5; DB 7; Length 327;
; Best Local Similarity 64.3%; Pred. No. 37; Mismatches 1; Indels 3; Gaps 1;
; Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
; GENERAL INFORMATION:
; APPLICANT: KIORA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
; FILE REFERENCE: 4093-13
; CURRENT APPLICATION NUMBER: US/11/165,226
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: JPP004-189007
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-11-165-226-62

RESULT 10
US-10-714-887-10
; Sequence Match 47.3%; Score 35.5; DB 7; Length 327;
; Best Local Similarity 64.3%; Pred. No. 37; Mismatches 1; Indels 3; Gaps 1;
; Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
Qy 1 KGGRKMLKSTRRQR 14
Db 120 QGGN--KSTRRQR 130

RESULT 11
US-11-165-221-52
; Sequence Match 48.0%; Score 36; DB 6; Length 280;
; Best Local Similarity 50.0%; Pred. No. 26; Mismatches 4; Indels 0; Gaps 0;
; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GGRKMLKSTRRQR 15
Db 20 GDRGLVPSTREER 33

RESULT 12
US-11-165-221-52
; Sequence Match 48.0%; Score 36; DB 6; Length 280;
; Best Local Similarity 50.0%; Pred. No. 26; Mismatches 4; Indels 0; Gaps 0;
; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GGRKMLKSTRRQR 15
Db 20 GDRGLVPSTREER 33

RESULT 13
US-11-165-221-52
; Sequence Match 47.3%; Score 35.5; DB 7; Length 327;
; Best Local Similarity 64.3%; Pred. No. 37; Mismatches 1; Indels 3; Gaps 1;
; Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CEBELMAN, Robert
; APPLICANT: RAYCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REBETTI, Peter
; APPLICANT: KOMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MB10058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 101412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 091506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 601135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 091394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 091533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 091533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 091532,591
; PRIOR APPLICATION NUMBER: 091532,591
; ORGANISM: Escherichia coli
; US-11-165-221-52

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PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/5533, 030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125, 814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713, 994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2053 polypeptide reference sequence; clade identifier
US-10-714-887-10

Query Match 46.7%; Score 35; DB 6; Length 342;
Best Local Similarity 42.9%; Pred. No. 47;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGKMLKSTRQR 15
Db 305 GGOKLQETREKKR 318

RESULT 11
US-11-024-959-410
Sequence 410; Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 04443-0360
CURRENT APPLICATION NUMBER: US/11/024, 959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533, 036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentIn version 3.3
SEQ ID NO 410
LENGTH: 441
TYPE: PRT
ORGANISM: Pinus radiata
US-11-024-959-410

Query Match 46.7%; Score 35; DB 7; Length 441;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 FGGRKMLKSTRQR 15
Db 124 KGG-SIKMTHHQKR 136

RESULT 12
US-10-453-372-852
Sequence 852; Application US/104533372
Publication No. US2006003333A1
GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453, 372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 852
LENGTH: 844
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-852

RESULT 13
US-10-453-372-856
Sequence 856; Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453, 372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 856
LENGTH: 844

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-453-372-856
 Query Match 46.7%; Score 35; DB 6; Length 844;
 Best Local Similarity 53.8%; Pred. No. 1.2e-02; 3; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 4;
 Qy 2 GGRKMLKSTRQR 14
 Db 825 GGRGOLHSRKQK 837

 Search completed: February 4, 2006, 03:47:59
 Job time : 11.5556 Secs

RESULT 14
 US-10-161-408-50
 Sequence 50, Application US/10161408
 Publication No. US20050287647A9
 GENERAL INFORMATION:
 APPLICANT: Perez, Carl
 APPLICANT: Fabijanski, Steven
 TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
 FILE REFERENCE: 24601-419
 CURRENT APPLICATION NUMBER: US/10/161,408
 CURRENT FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: US 60/294,687
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: US 60/296,329
 PRIOR FILING DATE: 2001-06-04
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: FastSBQ for Windows Version 4.0
 SEQ ID NO 50
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Integrase E174R
 US-10-161-408-50

Query Match 45.3%; Score 34; DB 6; Length 356;
 Best Local Similarity 50.0%; Pred. No. 74; 3; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy	2 GGRKMLKSTRQR 14	Db	267 GGETTIASTRRE 278
	:: :		:: :

RESULT 15
 US-11-69-041-162
 Sequence 162, Application US/11169041
 Publication No. US20060019284A1
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
 TITLE OF INVENTION: CELLS
 TITLE OF INVENTION: 10001 NP
 FILE REFERENCE: 10001 NP
 CURRENT APPLICATION NUMBER: US/11/169,041
 CURRENT FILING DATE: 2005-06-28
 PRIOR APPLICATION NUMBER: 60/584,405
 PRIOR FILING DATE: 2004-06-30
 NUMBER OF SEQ ID NOS: 527
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 162
 LENGTH: 543
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-169-041-162

Query Match 45.3%; Score 34; DB 7; Length 543;

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